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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

TITLE	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	SCMRPTAA	RESULT 1
Hamburger, J., Turetski, T., Kapeller, I. and Dereslewicz, R. Highly repeated short DNA sequences in the genome of Schistosoma mansoni recognized by a species-specific probe	Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma. 1 (bases 1 to 121)	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;	Schistosoma mansoni	S.mansoni (strain Egyptian) DNA, clone pSm1-7.		M61098.1 GI:161064	M61098	S.mansoni tandem repeat units.	SCMRPTAA 121 bp DNA linear INV 26-APR-1993		

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                                                                                                  Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhigh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kella, C., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macchen, C., Maddonald, P., Major, J., Marquis, N., Matthews, C., Macchen, C., Maddonald, P., Major, J., Marquis, N., Matthews, C., Macchen, C., Major, J., Marquis, N., Matthews, C., Macchen, C., Major, J., Marquis, N., Matthews, C., Macchen, C., Major, J., Marquis, N., Matthews, C., Marthews, C., Marthews, C., Marthey, M., Major, J., Martheys, C., Marthey, C., Major, J., Martheys, C., Martheys, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 69028)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Paylika Na, Canada, N., Bastien, V., Bloom, T., Boguslavkiy, L., Paylika Na, Canada, N., Bastien, V., Bloom, T., Boguslavkiy, L., Paylika Na, Canada, N., Bastien, V., Bloom, T., Boguslavkiy, L., Paylika Na, Canada, N., Bastien, V., Bloom, T., Boguslavkiy, L., Paylika Na, Canada, N., Bastien, V., Bloom, T., Boguslavkiy, L., Paylika Na, Canada, N., Bastien, V., Bloom, T., Boguslavkiy, L., Paylika Na, Canada, N., Bastien, V., Bloom, T., Boguslavkiy, L., Paylika Na, Canada, N., Bastien, V., Bloom, T., Boguslavkiy, L., Paylika Na, Canada, N., Bastien, V., Bloom, T., Boguslavkiy, L., Paylika Na, Canada, N., Bastien, V., Bas
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1 (bases 1 to 69028)
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McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Micol,R., Micoa,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
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Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainont,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 20, 2002 this sequence version replaced gi:14192963. All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
http://fir.genome.washington.edu/RM/RepeatMasker.html
Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SP6 end overlaps AC025211 [WICGR project L7840] by 111469 bp. are only submitting the final 69.0 kilobases (55.2 kb unique).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                     /rpt_family="Aludo"
complement(5102. .5229)
/rpt_family="FLAM_A"
6076. .6244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1786. .2113)
/rpt_family="MER1B"
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                 /rpt_family="THE1B" complement(7769. .8)
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                                                                                                                                                                                                                                                               complement(6280.
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                                                                                                                  complement(6914.
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2622. .3083
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complement/for
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/clone_lib="RPCI-11 Human Male
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/db_xref="taxon:9606"
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rpt_family="AluSx"
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56. .7720
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complement(19779. .20031)
/rpt_fam:1-
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/rpt_family="MIR"
complement(22559. .22615)
/rpt_family="L2"
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complement(21001
                                                                                                                       complement(23894.../rpt_family="MLTID"
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/rpt_family="LIPA10"
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/rpt_family="L1M4"
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            family="LIMEc"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 TCCGAAACCACTGGACGGATTTTTATGATGTTTGTTTTAGAGGCTTTGGTGACCTGCCTA 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grand-Pierre N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Lakoque, K., Lamazares, R., Landers, T., Leboczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
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McHdrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Direct Subrission, J., Zimmer, A. and Zody, M.
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (07-MAR-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
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Birren, B., Linton, L., 1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Lanazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
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Norbu, C., Norman, C., H., O'Connor, T., O'Donnell, P., O'Neell, D.,
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Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (08-SEP-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 8, 2001 this sequence version replaced gi:15431159.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://fitp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
Web site: http://www.seq.wi.mit.edu
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complement(21587. .21602)
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/note="<30 qual SNGL region"
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complement(20831. .2234>\
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complement(20691..20830)
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complement(20396. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="<30 qual SNGL region" complement(15859. .15865)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7486. .7679
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ACCESSION
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD 148641 TCTATATTCAGTTCAATCCTAATAAAAATTATTGAATTAATAAACTTATGCACTTAAAA 148700
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 TAATAAACGCTCTCGCACCCGCAATTATATTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 AAAATACTACAAACAAAATGATTATTTGCGAGAGCGTGGGCGTTAATATAAAACAAGAAC 201
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Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,
Donelan, J., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C.,
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Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P.,
Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.,
Meldrim, J., Wolla, M., Morris, W., Morrow, J., Mychalecky J.J.,
Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B.,
Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,
Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,
Wheeler, J., Wyman, D., Ye, W.J. and Zody, M.
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 186360)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP11-44H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 17, clone RP11-44H5, complete sequence.
                                                                                                                                                                                                                 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,
                                                                                                                                                                                                                                                                                                           Submitted (07-JUL-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Risback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuper,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,M., Subramanian,A., Talamas,J., Tesfaye,S., Thododre,J., Topham,K., Travers,M., Travis,N., Tilgilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Submitted (31-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on May 31, 2002 this sequence version replaced gi:5391470.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html Direct Submission Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L1066
Center clone name: 44_H_5 Center code: WIBR Web site: http://v ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research http://www-seq.wi.mit.edu

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complement/1="/
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/rpt_family="L2"
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/rpt_family="L2"
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/rpt_family="L2"
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/rpt_family="L1ME3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                               _family="MLT1K"
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                                                                                                 family="MIR"
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AC008106
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                                                                                           COMMENT
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Matches 105; Conserv
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                                                                                                                                                                                 Birren, B., Linton, I., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,
Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C.,
Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G.,
Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L.,
Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P.,
Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughilin, J.,
Meldrin, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J.,
Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B.,
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Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,
Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,
Wheeler, J., Wayman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATAAACTAACCCTCTAACACACTAATATAT 153340
Submitted (22-JUL-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Sep 4, 2000 this sequence version replaced gi:7329486. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218922 bp DNA linear HTG 04-SEP-2000 Homo sapiens chromosome 17 clone CTD-3008D3 map 17, WORKING DRAFT SEQUENCE, 34 unordered pieces.

ACO08106
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Birren, B. at Cromosome 17, clone CTD-3008D3
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                                                                                                                                                                        Direct Submission
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complement(29376.
/rpt_family="L2"
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complement(28786. .29090)
/rpt_family="L2"
29159. .29240
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3. .31415
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Pred. No. 0.76;
0; Mismatches 107;
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                        14183: contig of 1967 bp
14184 14283: gap of 100 bp
14284 17330: contig of 3047 bp 1
17331 1730: gap of 100 bp
17431 21134: contig of 3047 bp 1
17431 21134: contig of 3047 bp 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dy-pyimer-amersham; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 19717 bases at least Q40 Consensus quality: 201682 bases at least Q20 Consensus quality: 211643 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 4.1 in Q20 bases; agarose-fp Quality coverage: 3.8 in Q20 bases; sum-of-contigs
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Center clone name: 3008_D
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Insert size: 215622; sum-of-contigs
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43868 50104:
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39735 4376
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3 8474: contid of 5 8574
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6312: c
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7 12216: gap
                                                                                      54896: contig of 4692
54996: gap of 100 b
61677: contig of 6681
                                                                                                                                                                                                                                                                                                    100 b
24528: contig of 3194
24528: gap of 100 br
27705: con+'~ 7
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                                                                                                                                                                                                                  30206: gap of 100 bp in length 35366: contig of 5160 bp in length 35466: gap of 100 bp 39634: contig of 4168 bp in length
                                                                           61777: gap of
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                                             68142:
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50104: contig of 6237 bp
0204: gap of 100 bp
54896: contig of 4692 bp
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                                                          68042:
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10328: contig of 1754 bp
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.03: gap of 83935: contig of
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                                          42: contig of 6265
                                                                                                                                                                                                                                                                                                       p of 100 bp contig of 3177 b
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contig of 1500
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of 1011 bp
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= 12.
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183974 184073:
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                                                                                           /note="assembly_fragment" 50205. .54896
                                  /note="assembly_fragment"
61778. .68042
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27806. .30106
                                                                                                                            43868.
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/db_xref="taxon:9606"
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92731: contig of
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11655: gap of 100 bp
11655: gap of 100 bp
120772: contig of 9117 bp
120872: gap of
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143160: contig of 13191 bp
43260: gap of 100 bp
154541: contig of 11281 bp
54641: gap of 100 bp
170485: contig of 15844 bp
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218922: contig of
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200761: contig of 16688
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MIZINY D. M. Addins, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Simage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burchl, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnbart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Ganner, T., Garza, N., Gill, R., Gorrell, J.H., Gao, J., Garcia, A., Ganner, T., Garza, N., Gill, R., Gorrell, J.H., Guvara, W., Gunrathe, P., Hamilton, K., Grandez, J., Hodgson, A., Hogues, M., Hollows, A., Hernandez, J., Hodson, B., Jia, Y., Johnson, R., Jölivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Schurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC095286 171744 bp DNA linear HTG 11-JUL-2002 Rattus norvegicus clone CH230-12C16, *** SEQUENCING IN PROGRESS ***, 68 unordered pieces.
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84036. .92731
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143261. .154541
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111656. .120772
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92832. .102205
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76104. .83935
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Direct Submission

Submitted (16-5EP-2001) Human Genome Sequencing Center, Department

Submitted (16-5EP-2001) Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 171744)
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 68 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA On Jul 10, 2002 this sequence version replaced gi:17943590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished 2 (bases 1 to 171744)
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Direct Submission
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Center clone name: CH230-12C16
Center clone name: CH230-12C16
Center clone name: CH230-12C16
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 127827 bases at least Q40
Consensus quality: 127822 bases at least Q30
Consensus quality: 127822 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
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1396: contig of 1396 bp in length
1496: gap of unknown length
2649: contig of 1153 bp in length
2749: gap of unknown length
3906: contig of 1157 bp in length
4006: gap of unknown length
5016: contig of 1010 bp in length
5116: gap of unknown length
6328: contig of 1010 bp in length
6428: gap of unknown length
7854: contig of 1426 bp in length
7854: gap of unknown length
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COMMENT

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y of 1807

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                                               MO 63108, USA
4 (bases 1 to 57075)
Waterston, R.H.
Direct Submission
Submitted (18-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                                                                                                                                                                                                               2 (bases 1 to 57075)
Trani, L., Kozlowicz, A. and Elliott, G.
The sequence of Homo sapiens BAC clone RP11-321C7
Unpublished (2001)
                                                                                                                                                                                                                                                                          99063792
9847074
                                                                                                                                                           3 (bases 1 to 57075)
Waterston,R.H.
Direct Submission
Submitted (23-SEP-200) Genome
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Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
Waterston,R.

Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
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AC080073.6 GI:15638817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP4-736H5, 2000 bp overlap; the clone sequenced to the right is RP11-42LN10, 2000 bp overlap.
Actual start of this clone is at base position 109513 of RP4-736H5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Sep 18, 2001 this sequence version replaced gi:15487471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphisms have been indentified between AC005482 and AC080073
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Contact: sapiens@watson.wustl.edu
Summary Statistics
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1485. .1589
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2070. .2443
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/map="7"
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6611. .6786
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence of neurexin III gene in human chromosome
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join(<546. 624,56473. 57398)
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complement(12936. .13146)
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complement(50447. .50501)
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              complement(52039. .52067)
/rpt_family="POLY_A"
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/rpt_family="AluY"
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complement(34901. .35194)
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complement/losss
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complement/secc:
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***, 82 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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complement(62520. .62627)
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Worley,K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu/
Center project Information
Center project name: GQLI
Center clone name: CH230-133E1
Center clone name: CH230-133E1

Center clone name: CH230-135E1

Center clone name: CH230-135E1

Center clone name: CH230-135E1

Sequencing vector: Placanid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 60236 bases at least Q40
Consensus quality: 73589 bases at least Q30
Consensus quality: 80243 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 82 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.
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Migny D. M., Adams (C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alisbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barboroks, S.L., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buke, J., Burel, N.P., Burkett, C., Burell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chave, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Dany, Carvoil, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Cartell, J.R., Gazoti, A., Garner, T., Garza, M., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, M., Gill, R., Gorreill, J.H., Gavara, W., Gunrattne, P., Halle, S., Hamilton, K., Harris, K., Harris, K., Harlad, P., Halles, S., Hamilton, K., Hernandez, O., Hodyson, A., Horston, R., Holloway, C., Hollins, B., Hennandez, O., Hodyson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, J.C., Lewis, L., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, Y., Johnson, R., Julyk, S., Martindale, A., Martinez, E., Mahseshwari, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus clone CH230-9C3,
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7: gap of unknown length
7: gap of unknown length
9: contig of 2640 bp in length
9: contig of 2142 bp in length
9: gap of unknown length
5: contig of 1786 bp in length
5: gap of unknown length
3: contig of 2718 bp in length
3: contig of 2718 bp in length
9: gap of unknown length
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9: gap of unknown length
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*** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USB on Jul 10, 2002 this sequence version replaced gi:17942286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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Direct Submission
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 79 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number will be preserved.
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 119125 bases at least Q40
Consensus quality: 125091 bases at least Q30
Consensus quality: 130301 bases at least Q20
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                                                                                                                                                                                                                                                     2 (bases 1 to 32940)
Graves, T., Wohldmann, P. and Gillam, B.
The sequence of C. elegans cosmid F10D2
Unpublished (2001)
3 (bases 1 to 32940)
Waterston, R.
Direct Submission
Submitted (17-MAY-2002) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans Chromadorea; Rhabditida;
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF022972 32940 bp DNA linear INV
Caenorhabditis elegans cosmid F10D2, complete sequence.
AF022972
                 NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998) 99065613
                                                                                                                                                                                                                      Louis, MO 631
Submitted by:
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                                                                                                         Department of Genetics, Washington University St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CB10 IRQ, England email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                     Genome Sequencing Center
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10: contig of 2141 bp in length
10: gap of unknown length
10: contig of 2170 bp in length
10: gap of unknown length
10: contig of 2205 bp in length
10: contig of 2015 bp in length
10: contig of 1865 bp in length
10: gap of unknown length
11: contig of 2901 bp in length
12: contig of 2184 bp in length
13: contig of 2184 bp in length
14: contig of 3346 bp in length
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No. 3.
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INV 17-MAY-2002

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans cenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coding segences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The 5' cosmid is T01C4, 997 bp overlap; the 3' cosmid is F09 bp overlap. Actual start of this cosmid is at base position F10D2; actual end is at 6797 of F09G2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Hypothetical protein F10D2.3"
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/translation="MLLIHYVNLTHFKTSHNEFWLDLKVFLAIBCVLYFIDLFNMIFN
FVFLIKAHOFHRWEGCIYAWLFVINGTDNKALFXTW
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VTDKKNTVYLITFLLVIDGIALMLSCFLQWLKKRIYVRLEDNYVITSVLAQREQVAB
UNPTGKHHILLSGKHYEFGQMMNNVIYYMGFMNMTVLSVLESSEDLTFPHNTVITL
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EENTMSNHFDHLRDAWETNQGKGKFQYRTHHSKQKKEVSIEKFLKMIRFHNNAEPSEI
AWSCMSPISRCCGIGCCPKTSKSQSESIFHSVFGYMCGGFMFLCCLYLLLSLVMFLCN
sequence F10D2.4)"
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                                                                                                                                                                   complement(join(4273. .4373,4427. .4604,4712. .4837,
4883. .4957,5004. .5070,5123. .5257,5322. .5485,6169.
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                                                                                                                                                                                                                                                                                                        /note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=F10D2.4;class
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVWHRYIPWFPSSPRPTATPRSETHEMQELNPSTHRSPSRLHLAV"
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//genemipioo2.3"
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http://www.wormbase.org/db/seq/sequence?name=F10D2.3;class
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494. .3628
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/strain="Bristol N2"
/db_xref="taxon:6239"
/chromosome="V"
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                                                                                                           product="C.
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                                                                                 elegans STR-112 protein
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base position 798
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complement(join(7548. .7722,7838. .7933,8029. .8165,
8211. .8296,8419. .8606,8652. .8887,8954. .9096,9143. .9253,
9387. .9609,9655. .9888))
/gene="F10D2.5"
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GHNVTFFTPT1IRKFSKINYVKHTKHVIHLEPSEKLERYGNQMEDVDISRFWTDDSSM
AEMFPMIKLFNEMFAEQAFYLGQNLDVLDELKEMKFDVMIFERFAECAYFLLEYLEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="strong similarity to UDP-glucuronosyltransferases; coded for by the following C. elegans cDNAs: ykl172e10.3, ykl172e10.5"
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/gene="F10D2.6"
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TEAGHNVTLFSPTIIDEFRNYSYTKLIKDVAYLDPSPELKAIGDLIAGNKKWWNQEFS
VFEIPQTTRFFKSIIREQNNVLANNLALLOGLKQKKFDLILFESVFTCALPLWEYLEI
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http://www.wormbase.org/db/seg/sequence?name=F10D2.5;class
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vfycgfstwatirehrgasdrtrhlhrolfkalvfotlvpsitmyiptgvmfiafffd
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LMSFFSFFSIFYAIVESILRPIMHIENTTFFLISRKRFDYSTRLGKINSAFYCACFAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDTOLFASETENIHFSSWYDOTALLADRRUFAFFTHAGIGSVBNYSULGKESINGEIF
ADOMRNAKMARHNGSIEISKYDIGNGEKIEKTILFULFDSYSLISAEKLAROLANOF
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IAFTYLTVVLTIYSYLYFVLKFYASCLKAKIKTD"
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GSVNEVSYFGKPTIMCPLSGDQMRNAKMLERHNGSIEFSKYDLHNEKYVANAFRKILY
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MTPEYYQSYTNPEKKIYTLEKLSEASEIFMNSNPFLDFPRATITKNIQIGGISVNLDT
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/gene="F10D2.7"
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THEFKSFRPPYQAIDIQKMEHLSSFILSNSNPYIDYPRPTLEKNVQIGGISVDVENLK
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11262. .11347,11394. .11533,11579. .11951,12253. .12363,
12414. .12723,13107. .13250))
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http://www.wormbase.org/db/seg/seguence?name=F10D2.7;class
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/product="Hypothetical protein F10D2
/protein_id="AAC48237.1"
                                                                          /codon_start=1
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                                                                                                       note="strong similarity to UDP-glucuronosyltransferases"
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/translation="mililalletlyanyssfnflyfcplfahshskffatiadslfda ghnvafftplivekyrnfnytkstkdvvymepskkikbygromstgdfvriwtedsta telityvrlfokmyneggfvmkdnielindlkkrkedviifeafifsayplmdyleip

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Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Rarlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.C., Lewis, L.C., Liu, J., Li, Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mel, G., Metzker, M. Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.
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Rattus norvegicus clone CH230-81E15,
***, 59 unordered pieces.
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AC111374.2 GI:21735902
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus
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/gene="F10D2.12"
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DSSDEFAKGIENIHFAKWYPQTALLADSRLSAFLTHAGLGSTTELSYLGKPAILCPQL
FDQMRNTKMLYRHNGSIELSKYDLGKSEKIIEAFQAILFDSSYAKNAQKLAEQLENQP
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http://www.wormbase.org/db/seq/sequence?name=F10D2.12;clas
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5, *** SEQUENCING IN PROGRESS
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Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (13-7UL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 114473)
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Worley,K.C.
Direct Submission
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Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 69854 bases at least 040
Consensus quality: 74696 bases at least 030
Consensus quality: 78828 bases at least 020
                                                                                                                                                                                                                                                         Center project name: GMDD
Center clone name: CH230-81E15
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/doos/Genbank.draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 59 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. 2909 3009 4063 4163 5250 5350 6639 6739 1325 1425 10059 gap of unknown contig of 1087 contig of unknown contig of 1289 contig of unknown contig of 1053 gap of contig gap of contig gap of unknown contig of 1054 gap of unknown contig of 1484 contig of 1324 bp in length f unknown of 1020 f unknown of 1048 unknown of 1062 unknown length bp in] bp in l ni dq ď ni dq length bp in length ar da length length length Length length ij. u, length length length length length length length length

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                                                                                        Submitted (26-AUG-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA On Aug 26, 1999 this sequence version replaced gi:5668760. This sequence is derived from the two haplotypes of RPCI-11. No genes were found in this sequence.
                                                                                                                                                                                                                                            Submitted (08-MAY-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA 3 (Dases 1 to 177720) Seattle, WA 98195, USA 10 (Dases 1 to 177720) Bickhoff.R., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Rowen,L., Harrison,G., James,R., Lasky,S., Madan,A., Ratcliffe,A., Shaffer,T. and Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                            Rowen,L., Madan,A., Qin,S., Abbasi,N., Dors,M., Dickhoff,R., James,R., Loretz,C., Lasky,S., Madan,A., Prescott,S., Ratcliffe,A., Shaffer,T. and Hood,L.
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/db_xref="taxon:9606"
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                Bouck, J., Bowle, S., Bireva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Bscotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Escter, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Homsi, F., Howard, S., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Homsi, F., Howard, S., Hart, M., Haylak, P., Hawes, A., Hernandez, J.,
Homsi, F., Howard, S., Hart, M., Haylak, P., Hawes, A., Hernandez, J.,
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Homsi, F., Howard, S., Hart, M., Haylak, P., Hawes, A., Hernandez, J.,
Homsi, F., Howard, S., Hart, N., Haylak, P., Hawes, A., Hernandez, J.,
Li, J., Li, Li, J., Li, Li, J., Liu, M., Loulseged, H.,
Li, J., Li, Charge, O., Lieu, C., Liu, J., Liu, M., Loulseged, H.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E.,
Manneshwari, M., Mapua, P., Martin, M., Martinez, E.,
Manneshwari, M., Martinez, E., Wockend, M.P., Medaor, M., Mayen, N., Notzker, M.,
Moser, M., Nakerson, E., Wockend, S., Oguh, M., Okwnoni, G., N.,
Mguven, N., Nakerson, E., Wockend, S., Oguh, M., Okwnoni, G., N.,
Mguven, N., Nakerson, E., Respective, M., Serven, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus clone CH230-10D16, ***, 80 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
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/replace="t"
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/note="396NB: aaaaaagg; 209A20: g"
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   Nickerson, E., Nwokenkwo, S., Oguh, M.,
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Okwuonu, G.,
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Direct Submission
Direct Submission
Submitted (10-7UL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 30, 2002 this sequence version replaced gi:21629089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Waltlams, G., Williamson, A., Waeren, R., Washington, C., Watrington, S., Williamson, A., Wiley, R., Wooden, S., Wortey, K., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinston, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baylor Plaza, Houston, 3 (bases 1 to 190481)
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Direct Submission
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Sequencing vector: Plasmid; Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 109635 bases at least Q40 Consensus quality: 120858 bases at least Q30 Consensus quality: 126621 bases at least Q30 Consensus quality: 126621 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-helpebcm.tmc.edu
                                                                                                                                                                                                                                                                                 Center project name: GDNP Center clone name: CH230-10D16
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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

JOURNAL REFERENCE AUTHORS

TITLE

JOURNAL TITLE

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 80 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence. as soon as it is available and the accession number will be preserved. 9488 10820 10920 12014 12114 13224 9388 2981 4517 4617 6500 6600 8136 10919: 12013: 10819 contig of 1279 b gap of unknown I contig of 1501 b gap of unknown I contig of 1536 b gap of unknown I contig of 1883 b gap of contig y of 1332 unknown y of 1094 f unknown g of 1110 unknown of 1568 unknown of 1536 unknown of 1152 unknown 3 bp in length 6 bp in length 1 bp in length a length 5 bp in length a length length bp in l length length length bp in] length ni dq length bp in length length length length length length length

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CE 1 (bases 1 to 220181)

RS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbarda,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Barbarda,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Barbarda,J., Benton,J., Binage,K., Brown,M., Bryant,N.P., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Bouck,J., Charley,M.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,Z., Chowdhry,I., Christopoulos,C., Cler,G., Coyle,M.D., Dathorne,S.R., David,R., Chen,G., Chen,Z., Chowdhry,I., Dederich,D.A., David,R., David,R., David,R., David,R., David,R., David,R., David,R., David,R., Delaney,K.R., David,R., Dinh,H.H., Dedenay,K.R., David,R., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagy,N., Ford,J., Foster,P., Frantz,P., Falls,T., Ferraguto,D., Flagy,N., Ford,J., Foster,P., Frantz,P., Fabris,C., Harris,K., Hart,M., Havlak,P., Haues,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Hemsi,F., Howard,S., Huber,J., Havlyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Karlson,E., Martin,R., Morgan,M., Morris,S., Moser,M., Moser,M., Morris,S., Moser,M., Morris,S., Moser,M., Morris,S., Moser,M., Morris,S., Moser,M., Morris,S., Moser,M., Morris,S., Moser,M., Moser,M., Morris,S., Moser,M., Moser,M., Moser,M., Moser,M., Moser,M., Mos
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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83 unordered pieces.
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DNA linear HTG 08-JUL-2002
*** SEQUENCING IN PROGRESS ***,

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Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peerry,J., Perez,L.,
Peters,L., Dickens,R., Primus,B., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoshtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Tamerisa,K., Tang,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Sutton,A., Svatek,A., Tabor,P., Telfrod,B., Thomas,N., Thomas,S.,
Stansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,O.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wieczyk,R., Wooden,S., Worley,K.,
Williams,G., Williamson,A., Wieczyk,R., Wooden,S., Worley,K.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley,K.C. Direct Submission Direct Submission Sequencing Center, Department Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (08-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 7, 2002 this sequence version replaced gi:21700357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: hgsc-help@bom.tmc.edu

Center project name: GBLG
Center clone name: CH230-5J4
Center clone name: CH230-5J4

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Hig Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 144990 bases at least Q40
Consensus quality: 152139 bases at least Q30
Consensus quality: 157114 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 83 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence soon as it is available and the accession number will be preserved.
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of 1068
unknown
of 1322
     f unknown
g of 1603
f unknown
f unknown
f unknown
g of 1919
f unknown
f unknown
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f unknown
g of 2034
f unknown
g of 1807

3 bp in length
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of 1523
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of 1418

unknown of 1879

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Search completed: May 12, 2003, 01:46:42 Job time : 1711 secs
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72422: gap of unknown length
74890: contig of 2468 bp in length
74990: gap of unknown length
77937: contig of 2947 bp in length
7837: gap of unknown length
80271: contig of 2234 bp in length
80271: gap of unknown length
80371: gap of unknown length
83452: contig of 3081 bp in length
83452: contig of 3101 bp in length
83452: gap of unknown length
83455: gap of unknown length
84865: gap of unknown length
87355: gap of unknown length
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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240
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18.4
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/SIDS2/gcgdata/geneseq/geneseqn-embl/MA1990.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/MA1995.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/MA1990.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/MA1990.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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    120
6494
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  AAI70400
AAA46170
AAS46564
ABM60970
ABL17578
ABL17578
AAQ75857
AAX61476
                                                                                                                                                                                                                                                       SUMMARIES
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1279.025 Million cell updates/sec
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                                                                                                                                                                                             Description
Haemolysin regulat B. burgdorferi ant B. burgdorferi ant
                                                      Drosophila melanog
Drosophila melanog
                                                                                              Tumour suppressor
Human cancer relat
                                                                                                                                  Schistosoma manson GFP-Sml-7 fusion p
                                                                                                                                  ש
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10951
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                                                                        AAT58840
ABV54682
ABN68671
AAK85566
AAF18094
                                                                                  AAC59153
AAX20262
ABQ67094
                                                                                                 AAS20800
ABQ70115
ABQ71100
                                                                                                                           AAK79983
AAI62708
                                                                                                                                      ABN66701
AAL07031
AAK79984
AAL62709
AAL07030
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AAD14604
AAD14601
AAD14602
ABN70879
                     AAH29873
AAA57948
                                              AAK85565
AAK85567
                                                                                                                 ABL13398
AAS46340
                               ABQ33363
                                    ABQ33362
                                          ABQ67149
                    Human immune/haema
Human angiogenesis
Oligonucleotide fo
Oligonucleotide fo
C albicans apoptos
5611 bp Candida al
Buchnera sp. genom
Human ORFX ORF2412
Human nervous syst
          Human immune syste
Buchnera sp. genom
                                                    Human immune/haema
                                                              Human immune/haema
                                                                   Streptococcus poly
                                                                        Human angiogenesis
Mycoplasma genital
Human prostate exp
                                                                                       Human secreted pro
Borrelia burgdorfe
                                                                                                     Tumour suppressor
Clostridium diffic
Listeria monocytog
                                                                                                                     Human immune/haema
Human breast or ov
Drosophila melanog
                                                                                                                                           Human
                                                                                                                                                 Human
                                                                                                                                                     Streptococcus poly Human reproductive
                                                                                                                                                                Streptococcus poly
                                                                                                                                                                          Dengue virus (DEN)
Dengue virus (DEN)
Wild-type, virulen
                                                         Lung cancer associ
                                                                                                                                      Human reproductive
                                                                                                                                                                     Attenuated, vaccin
                                                                                            Listeria monocytog
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ALIGNMENTS

RRSULT 1
AAJ704
AAJ704
AAJ70
A 04-APR-2000; 2000BR-0001536. 04-APR-2001; 2001WO-BR00035 11-OCT-2001. Schistosoma mansoni repeater unit DNA. 07-JAN-2002 (first entry) AAI70400; AAI70400 standard; DNA; 120 (FICC-) FICCRUZ FUNDACAC CRUZ OSWALDO. WO200175148-A1 primer_bind primer_bind Schistosomiasis; infection; diagnosis; Schistosoma mansoni. /note= "primer of AAI70401" 91..110 Location/Qualifiers complement (1..19) "primer of AAI70402" Ь BP. ds.

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RESULT 2
AAA46170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of a highly repeated short DNA sequence in the genome of Schistosoma mansoni. PCR primers (see AAI70401 and AAI70402) that flank this sequence are used in the method of the invention for diagnosing Schistosoma infection. The method involves collection of the sample to be examined, extraction of Schistosoma sp. DNA, amplification by PCR, separation of PCR products by electrophoresis, and detection e.g. by colouring with silver salts. A kit for diagnosing infection, which includes the primers, is claimed. The method is useful for detecting schistosoma sp. parasites by detecting the DNA of the parasite in a biological sample. It is especially useful in cases of low infection intensity for which parasitological stool tests
                                                                                                                                                                                                              GFP-Sm1-7 fusion construct; circular; green fluorescent protein; glutathione S-transferase; eukaryotic diploid multicellular parasite; universal graft; transgenic eukaryotic parasite; acquired deficiency; genetic deficiency; hormone deficiency; metabolic deficiency; haematcological deficiency; immunological deficiency; immunotherapy; anti-microbial therapy; anti-cancer therapy; drug addiction; poisoning condition; geriatric condition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing infection by parasites of the Schistosoma sp. in a biological sample especially used in cases of low infection intensity, comprises detecting a specific region of the DNA of Schistosoma by polymerase chain reaction -
 Eukaryotic diploid multicellular parasite useful for in vivo delivery of beneficial gene products involves transformation with a transgene -
                                                                                                         01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                  AAA46170 standard; DNA; 6494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 120 BP; 36 A; 20 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
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                                                               Hamburger
                                                                                    (YISS ) YISSUM RES & DEV CO
                                                                                                                              01-DEC-1999;
                                                                                                                                                    08-JUN-2000
                                                                                                                                                                        W0200032804-A1
                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                         27-SEP-2000
                                                                                                                                                                                                                                                                                                                                               AAA46170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             demonstrate little sensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                   2000-412348/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page
                                                               Ţ
                                                                                                                                                                                                                                                                                                     fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                        .(first entry)
                                                               Laban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; 34pp; English.
                                                                                                         98US-0201850
                                                                                                                              99WO-IL00651.
                                                                                                                                                                                                                                                                                                   protein construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dias Neto
                                                               A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.4%;
93.9%;
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ficial gene products a transgene -
                                                                                                                                                                                                                                                                                                                                                                  ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44.2;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 G; 38 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pontes LA;
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          in humans and animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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Example 2; Fig 6; 90pp; English.

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XX

This sequence represents a GFP-Sm1-7 fusion construct contained within a cc recombinant vector. This sequence contains the green fluorescent protein cc (GFP) coding sequence from Aequorea victoria, and the C promoter sequences from Neguorea victoria, and the C promoter sequences. The invention relates to a entaryotic diploid multicellular parasite transformed with a transgene. Transgenic cc entaryotic parasites are useful as universal grafts for in vivo delivery cc of beneficial gene product in humans and animals. The parasites can particularly be used for restoration of deficiencies whether acquired or cc genetic, such as hormone deficiencles, metabolic deficiencies, famunological deficiencies, immunotherapy, cc anti-microbial therapy, anti-cancer therapy. They can also be used for treatment of drug addiction, of poisoning conditions, and for amelioration of geriatric conditions. Treatment of humans with in vivo cc transgenes are universally compatible, readily available and inexpensive. Genotypic alterations of the patients is avoided, reducing risks of culturagenesis and malignant transformation.

XX Sequence 6494 BP; 1754 A; 1373 C; 1481 G; 1886 T; 0 other;
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RESULT 3
AAS46564/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
15-MAR-2000; 2000DE-1013847.
06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                      Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                           Tumour suppressor gene derived chemically modified sequence #286
                                                                                                                                                                                                                                                                                                                                                                                                                        AAS46564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS46564 standard; DNA; 6134 BP.
                                                                                                                   15-MAR-2001; 2001WO-EP02955
                                                                                                                                                                                            WO200168912-A2
                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                    cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2001
                                                                           15-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 CTCCGAAACCACTGGACGGATTTTTATGATGTTTGTTTTAGATTATTTG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCGAAACCACTGGACGGATTTTTATGATGTTTGTTTTAGAGGCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.4%; 93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44.2;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6494;
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Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. cancer

Claim 1;

SEQ

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No 286;

27pp; English

01ek

(EPIG-)

EPIGENOMICS :
Piepenbrock

AG

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Berlin

WPI; 2001-602752/68.

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RESULT 4
ABN60970
ID ABN6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            533 genomic sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA, (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences
16-AUG-2000; 2000US-226326P
                                                    16-AUG-2001; 2001WO-US25840.
                                                                                                           21-FEB-2002
                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                           Human cancer related polynucleotide SEQ ID NO 937
                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABN60970 standard; cDNA; 581 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6134 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the
                                                                                                                                                               WO200214500-A2
                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is missing).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 CGTTAATATAAAACAAGAACTAATAAACGCT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ATCTGAATCCGACCAACCGTTCTATGAAAATCGTTGTATCTAGACTTAGGCTGGTTGGCA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGCTTTGGTGACCTGCCTAAAAATACTACAAAATGATTATTTGCGAGAGCGTGGG 181
                                                                                                                                                                                                                                                                       therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATTAATTCAAAACAAATAAAAATAAAAACT 3759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGATACTTTTAGCAACATACTCCGAAAACCACTGGACGGATTTTTATGATGTTTTGTTTTAG 121
                                                                                                                                                                                                                                                                                                    cytostatic; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1913 A; 76 C; 1273 G; 2872 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.2%;
                                                                                                                                                                                                                                                                             tumour;
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Pred. No. 0
                                                                                                                                                                                                                                                                             gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 109;
                                                                                                                                                                                                                                                                          gene mapping; tissue profiling;
ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid for producing a polypeptide, detecting expressed genes correlated with a cancerous state of a \mathfrak n and inhibiting tumor growth -
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Lamson G, S
                                                                                                                                                                                                                                  pharmaceutical; gene; ds
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                       New isolated nucleic acid genes from Drosophila and interactions -
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nilarity 57.5%;
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(USSH ) US DEPT HEALTH & HUMAN SERVICE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemolysin regulator; tuberculosis; vaccine; antisense; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemolysin regulator DNA.
                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
24-MAY-1993;
                                 25-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 GTTTGTTTTAGAGGCTTTGGTGACCTGCCTAAAAATACTACAAACA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 GCTGGTTGGCAAGATACTTTTAGCAACATACTCCGAAACCACTGGACGGATTTTTATGAT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Similarity
61; Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4207; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry
93US-0066830
                                 94WO-GB05869.
                                                                                                                                                                                                                                          47..52
/*tag=
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99..101
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76..81
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                                                                                                                                                                                                                                                                      c
"5/6 match with E. coli promoter -10 consensus sequence (TATAAT)"
                                                                                                                                                                                                                                                                                                                                                                                                     "haemolysin regulator"
                                                                                                                                      "4/8 match with (AGGAAAGG)"
                                                                                                                                                                                                          "4/6 match with (TTGACA)"
                                                                                                                                                                                                                                                                                                                                                   "translation start codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₿₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.2;
                                                                                                                                                                                                                           <del>-</del>35
                                                                                                                                                       RBA binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23; Length 7729;
                                                                                                                                                                                                                           consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT 8
AAX61476
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression. DNA fragments can be used as probes for antisense therapy to inhibit haemolysis, and the protein regulator gene itself may be used as an immunogen for vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               King
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain, to generate humoral and cellular responses against Mycobacterium tuberculosis. Non-coding sequences may be coupled reporter genes to screen for compounds that increase gene
                                                                                                  (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                     AAX61476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX61476 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1020 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence encodes the E. coli haemolysis protein regulator gene which may be used, in an avirulent Mycobacterium bovis BCG vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding carbapenem R gene product carbapenem antibiotics in bacteria and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAR67645
New isolated Borrelia burgdorferi nucleic acids
                                                                     Choi GH,
                                                                                                                                                                                     03-SEP-1997;
                                                                                                                                                                                                                                              30-DEC-1998.
                                                                                                                                                                                                                                                                          W09859071-A1
                                                                                                                                                                                                                                                                                                                                Antigenic
                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-1999
                              P-PSDB; AAY19780
                                           WPI; 1999-189980/16.
                                                                                                                                           22-JUL-1997;
                                                                                                                                                          20-JUN-1997;
22-JUL-1997;
                                                                                                                                                                                                                  18-JUN-1998;
                                                                                                                                                                                                                                                                                                   Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 CCGCA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
                                                                                                                                                                                                                                                                                                                                                           burgdorferi antigenic protein coding sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1995-022809/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGATTATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAAACGCAATCGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGATTATTTGCGAGAGCGTGGGCGTTAATATAAAACCAAGAACTAATAAAACGCTCTCGCAC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATTTATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTAAAGAGGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68;
                                                                                                              HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                  MEDIMMUNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 38-39; 46pp;
                                                                    Erwin AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sathish M,
                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                         97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 A; 195 C; 217 G; 260 T; 0 other;
                                                                                                                                                                                                                                                                                                                                vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA; 3363
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                                                                     Hanson MS,
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                                                                                                                                                                                                                                                                                                                                Lyme
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Pred. No. 2.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                disease;
                                                                     Lathigra R;
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    used for production

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                                                                                                                                                                                                                                                                                                                                infection; detection;
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                                                                                                                                                                                                                                                                                                                                                           t12.nt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1020;
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develop
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PARASOLT 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B. burgdorferi antigenic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3363 BP; 1193 A; 388 C; 505 G; 1277 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 58-59; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides
                                                                                                                                       New isolated Borrelia burgdorferi nucleic acids - us products for the diagnosis, prevention and treatment caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX61475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX61475 standard;
                                                                                  Claim 1; Page 57-58; 275pp; English.
                                                                                                                                                                                                                                                          WPI; 1999-189980/16.
P-PSDB; AAY19779.
                                                                                                                                                                                                                                                                                                                                          Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 GCTGGTTGGCAAGATACTTTTAGCAACATACTCCGAAACCACTGGACGGATTTTTATGAT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACAGAATAGTCCTTAATAAGAACTCTAAAAAACTTTATGCTATTGGA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGAGCGTGGGCGTTAATATAAAACAAGAACTAATAAACGCTCTCGCA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAAGAGTTAATATCTTGGTTGAAGATATTAAAGAAAATAAAAAGCACAATATTAAAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Similarity
84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               HUMAN GENO
                                                                                                                                                                                                                                                                                                                                       Erwin AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
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milarity 50.0%;
Conservative
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97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
                                                                                                                                                                                                                                                                                                                                          Hanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lуme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coding sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease;
                                                                                                                                                                                                                                                                                                                                          Lathigra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
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                                                                                                                                                                        ment of
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                                                                                                                                                                        to develop
diseases
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RESULT 10
AAD14603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flavivirus; avirulent;
structural protein genes or a second immunogenicity but These chimeric viruses elicit pronounced immunogenicity but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can albe used for detection of members of the Borrelia genus.
                           flavivirus. Chimeric viruses containing the attenuation mutated non-
structural genes of the virus are used as a backbone into which the
structural protein genes of a second flavivirus strain are inserted
                                                                                                                                   Chimeric flaviviruses that are avirulent and immunogenic, vaccinating against a range of dengue viruses -
                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD14603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD14603 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3441 BP;
                                                                                 The invention relates to avirulent,
                                                                                                                                                                                                                    Kinney
                                                                                                                                                                                                                                                                                                  16-FEB-2001; 2001WO-US05142
                                                                                                                                                                                                                                                                                                                             23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                      WO200160847-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dengue virus
                                                                     comprising
                                                                                                           Example 1;
                                                                                                                                                                                                                                            (USSH ) US
                                                                                                                                                                                                                                                                        16-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 GCTGGTTGGCAAGATACTTTTAGCAACATACTCCGAAACCACTGGACGGATTTTTATGAT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                         2001-497162/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACAGAATAGTCCTTAATAAGAACTCTAAAAAACTTTATGCTATTGGA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGAGCGTGGGCGTTAATATAAAACAAGAACTAATAAACGCTCTCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAAGAGTTAATATCTTGGTTGAAGATATTAAAGAAAATAAAAAGCACAATATTAAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGATAATCTTGAAAATTTCACTTATGGACTTACTAAAGATGAAAGTATTATTTTGAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84:
                                                                                                                                                                                                                    RM,
                                                                                                                                                                              AAE07982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                    ion relates to avirulent, immunogenic flavivirus chimeras amino acid mutations in the non-structural proteins of a
                                                                                                          Page 155-170; 470pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Dengue virus type I.
Dengue virus type II
                                                                                                                                                                                                                                             DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogenic; viral
                                                                                                                                                                                                                   Kinney CYH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dengue virus; DEN; vaccine; infection; virucidal; immunogenic; viral disease; pharmaceutical; chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                        2000US-0182829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEN)-2/1-VP chimeric cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 97..10272
                                                                                                                                                                                                                                                                                                                                                                              /product= "DEN-2/1-VP fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1219 A; 396 C; 513 G; 1313 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10723
                                                                                                                                                                                                                   Butrapet S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33.6;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                           English
                                                                                                                                                                                                                    Gubler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
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                                                                                                                                                                                                                   DL,
                                                                                                                                                                                                                                                                                                                                                                              protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                 Bhamarapravati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3441;
                                                                                                                                                  useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
     chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                  tot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                    Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes dengue virus (DEN)-2/1-vp fusion protein related to the invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone comprising a valine at the non-structural protein (N33)-250 and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capsid protein (C), premembrane/membrane protein (prM) and an envelope protein (E) from wild-type DEN-1 16007 virus.
                                                             Chimeric flaviviruses that are avirulent and immunogenic, vaccinating against a range of dengue viruses -
                                                                                                                                                                                        16-FEB-2000; 2000US-0182829
                                                                                                                                                                                                                 16-FEB-2001; 2001WO-US05142
                                                                                                                                                                                                                                        23-AUG-2001.
                                                                                                                                                                                                                                                                WO200160847-A2
                                                                                                                                                                                                                                                                                                                                                                                         aviruLent;
                                                                                                                                                                                                                                                                                                                                                                                                      Flavivirus;
                                                                                                                                                                                                                                                                                                                                                                                                                            Dengue virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD14604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD14604 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10723 BP; 3514 A; 2229 C; 2722 G; 2258 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flaviviruses are combined in a pharmaceutical composition to confer
                                                                                                                                                               ( HSSU ) US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 GAAAATCGTTGTATCTAGACTTAGGCTGGTTGGCAAGATACTTTTAGCAACATACTCCGA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTACAAACAAATGATTATTTGCGAGAGCGTGGGCGTTAATATAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGCCAAGGACCCATGAAATTGGTGATGGCTTTCATAGCATTCTTAAGATTTCTAGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACCACTGGACGGATTTTTATGATGTTTGTTTTAGAGGCTTTGGTGACCTGCCTAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAAACCGCGTGTCAACTGTTTCACAGTTGGCGAAGAGATTCTCAAAAGGATTGCTCTC
                                                                                                 2001-497162/54.
)B; AAE07983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCCCCAACAGCAGGAATTTTGGCCAGATGGGGCTCATTCAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84;
                                                                                                                                       RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                               DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                    Dengue virus
Dengue virus
                                                                                                                                                                                                                                                                                                                                                                                         immunogenic;
                                                                                                                                      Kinney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Dengue virus;
                                                                                                                                                                                                                                                                                                                                                                                                                            (DEN) -2/1-VV chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 97..10272
                                                                                                                                                                                                                                                                                         /product= "DEN-2/1-VV
                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                       CYH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.0%;
                                                                                                                                                                                                                                                                                                                                                    type
type
                                                                                                                                                                                                                                                                                                                                                                                         viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10723
                                                                                                                                      Butrapet S,
                                                                                                                                                                                                                                                                                                                                                                                                      DEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33.6; Di
Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                     H.F
                                                                                                                                                                                                                                                                                                                                                                                         disease;
                                                                                                                                                                                                                                                                                                                                                                                                      vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA
                                                                                                                                                                                                                                                                                         fusion protein"
                                                                                                                                      Gubler DL,
                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                      infection; virucidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 10723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                      Bhamarapravati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320
                                                                                                                                                                                                                                                                                                                                                                                          chimeric;
                                                                          useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                          for
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                                                                                                                                                                                                                                                                                                                                                                                            SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212
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The invention relates to avirulent, immunogenic flavivirus chimeras

comprising amino acid

Example 1;

Page 179-195; 470pp;

English

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AAD14601
ID AAD
QΨ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         덩
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DRN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone comprising a valine at the non-structural protein (NS3)-250 and the capsid protein (C), premembrane/membrane protein (prM) and an envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flavivirus; Dengue virus-1; DEN-1; vaccine; infection; virucidal; avirulent; immunogenic; viral disease; pharmaceutical; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes dengue virus (DEN)-2/1-VV fusion protein related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wild-type,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD14601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD14601 standard; cDNA; 10735 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10723 BP;
           Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccinating against a range of dengue viruses -
                                                                                                                     Kinney RM,
                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                          16-FEB-2000; 2000US-0182829
                                                                                                                                                                                                                            16-FEB-2001; 2001WO-US05142
                                                                                                                                                                                                                                                                 23-AUG-2001.
                                                                                                                                                                                                                                                                                                   WO200160847-A2
                                                                                                                                                                                                                                                                                                                                                                                                                        Dengue virus type I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 ACTACAAACAAAATGATTATTTGCGAGAGCGTGGGCGTTAATATAAAA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 GAGAAACCGCGTGTCAACTGTTTCACAGTTGGCGAAGAGATTCTCAAAAGGATTGCTCTC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCCCCAACAGCAGGAATTTTGGCTAGATGGGGGCTCATTCAAGAAGAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGCCAAGGACCCATGAAATTGGTGATGGCTTTCATAGCATTCTTAAGATTTCTAGCCAT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACCACTGGACGGATTTTTATGATGTTTTGTTTTAGAGGCTTTGGTGACCTGCCTAAAAAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAAATCGTTGTATCTAGACTTAGGCTGGCTTGGCAAGATACTTTTAGCAACATACTCCGA 86
                                                                                    2001-497162/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84;
                                                                   AAE07980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (E) from the vaccine strain of Dengue-1 (DEN-1) PDK-13 virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virulent DEN-1 16007 cDNA
                                                                                                                   Kinney CYH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 95..10273
                                                                                                                                                                                                                                                                                                                                  /product= "DEN-1 16007 protein"
                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3514 A; 2228 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.0%;
                                                                                                                   Butrapet S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33.6; D
Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2722 G; 2259 T; 0 other;
                                                                                                                     Gubler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 10723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84;
                                                                                                                     DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                   Bhamarapravati
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Structural genes of the virus are used as a backbone into which the structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. Crahese chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic CC flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present CDNA csequence encodes wild-type, virulent dengue-1 (DEN-1) 16007 virus protein used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1) CDEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome contains 5 non-coding region followed by a capsid protein (C) encoding region, followed by the region encoding non-contains proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3' conscious decimal proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 106-122; 470pp; English
                                                             non-coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to avirulent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenic flavivirus chimeras
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В Qy Ď, δÃ 뮍 δλ Matches Query Match Best Local 271 147 151 GAGAAACCGCGTGTCAACTGTTTCACAGTTGGCGAAGAGATTCTCAAAAGGATTGCTCTC 210 87 27 GAAAATCGTTGTATCTAGACTTAGGCTGGTTGGCAAGATACTTTTAGCAACATACTCCGA ACTACAAACAAATGATTATTTGCGAGAGCGTGGGCGTTAATATAAAA 194 ACCCCCAACAGCAGGAATTTTGGCTAGATGGGGCTCATTCAAGAAGAA 318 AGGCCAAGGACCCATGAAATTGGTGATGGCTTTCATAGCATTCTTAAGATTTCTAGCCAT 84; Similarity Conservative 14.0%; 50.0%; 0; Score 33.6; Pred. No. 4. Mismatches 84; DB 22; Indels Length 10735; 0; Gaps 86 270 0;

Sequence 10735 BP; 3432 A; 2232 C; 2774 G; 2297 T; 0 other;

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RESULT 13
AAD14602
                                                                                                   Flavivirus; Dengue virus-1; DEN-1; vaccine; infection; virucidal; mutein;
avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
                                                                                                                                                                                                                        01-NOV-2001
        mutation
                          mutation
                                                                                 mutation
                                                                                                                                                                                                      Attenuated, vaccine-strain DEN-1 PDK-13 variant cDNA
                                                                                                                                                                                                                                          AAD14602;
                                                                                                                                                                                                                                                             AAD14602 standard; cDNA; 10735 BP
                                              mutation
                                                              mutation
                                                                                                                                        Synthetic.
                                                                                                                                                Dengue virus
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(1567, A)
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                                           Å
                                                                                          protein variant"
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Qy
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                                                                               δÃ
                                                                                                                                                                                                     CC flavivirus. Chimeric viruses containing the attenuation mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEW-1, DEW-2, DEW-3 and DEW-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC confer simultaneous protection against infections. The present cDNA
CC sequence encodes attenuated dengue-1 (DEW-1) PDK-13 virus protein variant
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEW-1)
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC cretin (E) encoding region, followed by the region encoding on-
CC structural proteins (NS1-NS2A-NS2A-NS4A-NS4B-NS5) and finally a 3'
CC sequence contains (NS1-NS2A-NS2A-NS4A-NS4B-NS5) and finally a 3'
 B
                                                                                                            Query Match
Best Local S
Matches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric flaviviruses that are avirulent and immunogenic, useful vaccinating against a range of dengue viruses -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-FEB-2000; 2000US-0182829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-2001; 2001WO-US05142
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                                                                                                                                                                  Sequence 10735 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 130-146; 470pp; English.
                                                                                                                                                                                             non-coding region.
 211
                                                      151
                           87
                                                                        27 GAARATCGTTGTATCTAGACTTAGGCTGGTTGGCAAGATACTTTTAGCAACATACTCCGA 86
AGGCCAAGGACCCATGAAATTGGTGATGGCTTTCATAGCATTCTTAAGATTTCTAGCCAT 270
                        AACCACTGGACGGATTTTTATGATGTTTGTTTTAGAGGCTTTGGTGACCTGCCTAAAAAT 146
                                                    GAGAAACCGCGTGTCAACTGTTTCACAGTTGGCGAAGAGATTCTCAAAAAGGATTGCTCTC 210
                                                                                                             84;
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                                                                                                                        Similarity
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50.0%;
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                                                                                                            0;
                                                                                                                        Score 33.6;
Pred. No. 4
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                                                                                                             Mismatches
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                                                                                                             Indels
                                                                                                                                       Length 10735;
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35 TTGTATCTAGACTTAGGCTGGGTTGGCAAGATACTTTTAGCAACATACTCCGAAACCACTG

Best Lo Query Match

Local

Similarity

13.9%;

Score 33.4; D Pred. No. 3.3; 0; Mismatches

Conservative

0;

66; 24; 0 other;

Indels Length

Gaps

0;

94

1860; 0;

Sequence 1860 BP; 619 A;

296

C; 407

G; 538 Τ;

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ARESULT 14
ARM7082
XX ABN708
XX ABN708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                   Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds (I). A composition comprising (I) or a nucleic acid encoding (I), may used as a vaccine or diagnostic composition. The disease caused by used as a vaccine or diagnostic composition. The disease caused by
                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus progenes), comprising one of 5483 sequences (51), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABM56044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 4093; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-2000; 2000GB-0026333
24-NOV-2000; 2000GB-0028727
07-MAR-2001; 2001GB-0005640
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                                                                                                                          Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tettelin
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                                                                                                        chromatography,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-352536/38.
DB; ABP30248.
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                                                                                                     immunoassays,
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                                                                                                        and distinguishing/identifying
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95 GACGGATTTTTATGATGTTTTAGAGGCTTTGGTGACCTGCCTAAAAATACTACAAA 154

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RESULT 15
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                                                                    streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

(Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
the specification. The proteins have antibacterial and antiinflammatory
cactivity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
antibodies that bind (I) are used in the manufacture of medicaments for
the treatment or prevention of infection or disease caused by
Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.
Nucleic acids encoding (I) are used to determine whether a compound binds to
biological sample. (I) is used to determine whether a compound binds to
(I). A composition comprising (I) or a nucleic acid encoding (I), may be
used as a vaccine or diagnostic composition. The disease caused by
Streptococcus that is prevented or treated may be meningitis. Nucleic
acid encoding (I) may be used to recombinantly produce (I) and may be
used in gene therapy. Antibodies to (I) are used for affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
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P-PSDB; ABP26070.
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
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Sequence 1950 BP; 656 A; 309 C; 428 G; 557 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                        The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 3287-3288; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Telford J, Masignani V, Margarit Ros YI, Tettelin H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1039 GTGGATTTTCTAATAGGAATCGATTGAAAGCTTCGCTAAAGAGACGATTTGTAATTTTAA 980
                                                        chromatography,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENO-) INST GENOMIC RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                        immunoassays, and distinguishing/identifying
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Query Match

13.9%; Score 33.4; DB 24; Length 1950;

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Search completed: May 12, 2003, 01:14:51 Job time : 434.571 secs
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                                                                                                                                                                                                                                                                                           Best Local Similarity 52.5%; Matches 73; Conservative
                                                                                                                                             1129
                                                                                                                                                                                                                    1189
                                                                        1069 CAACTTCAGAATTTCCAAG 1051
                                                                                                         155 CAAAATGATTATTTGCGAG 173
                                                                                                                                                                                  95
                                                                                                                                                                                                                                                       35
                                                                                                                                                                                                                                       TIGIATCIAGACITAGGCIGGTIGGCAAGATACITTIAGCAACATACICCGGAAACCACIG 94
                                                                                                                                             GTGGATTTTCTAATAGGAATCGATTGAAAGCTTCGCTAAAGAGACGATTTGTAATTTTAA 1070
                                                                                                                                                                                GACGGATTTTTATGATGTTTTTAGAGGCTTTGGTGACCTGCCTAAAAATACTACAAA 154
                                                                                                                                                                                                                  TIGCTGCAATACGGGCTTTAGATGCCAAAATTCCTTTTTCAACAATCTTCTTAGCTACTT 1130
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                           Pred. No. 3.4;
0; Mismatches
                                                                                                                                                                                                                                                                                           66;
                                                                                                                                                                                                                                                                                           Indels
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Minimum DB seq length: 0
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Perfect score:
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                       Issued_Patents_Nh:*

1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    May 12, 2003, 01:08:23; search time 105.429 seconds (without alignments) 698.126 Million cell updates/sec
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Match Length
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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Dackfiles1.seq:*
                                                                                                             DB
US-08-557-115-2

PCT-US94-05869-2

US-08-325-426B-1

US-08-280-690-1

US-08-464-339A-1

PCT-US94-14388-1

US-09-345-882-1

US-09-345-882-1

US-09-345-882-1

US-09-889-718-1

US-08-184-099-183

US-08-184-099-187

US-08-185-65-398-39

US-08-185-65-398-39

US-08-185-65-398-39

US-08-185-65-398-39

US-08-185-65-398-39

US-08-185-65-398-39

US-08-195-101-3

US-08-195-273-39

US-08-967-101-66

US-08-967-101-66

US-08-967-101-66

US-09-127-480-66

US-09-127-480-66
                                                                                                                                                                                                                                                                     Sequence 1, Appli
Sequence 9, Appl
Sequence 1, Appli
Sequence 83, Appl
Sequence 83, Appl
Sequence 127, App
Sequence 39, Appl
Sequence 127, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
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sequence
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127, App
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US-08-557-115-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
  FEATURE:
                                                                                                                                                             ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 191 Pe
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Georgia COUNTRY: U.S.A. ZIP: 30303
                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                          E. coli
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27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.6	27.6	27.6	27.6	27.8	27.8	28	28	28
11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.5	11.5	11.5	11.5	11.6	11.6	11.7	11.7	11.7
5099	5099	5099	5099	5099	5099	5099	5099	921	11309	7425	3418	1630	1700	1700	4184	1049	448
4	4	w	ω	N	N	N	μ.	4	4	42	4	4	ω	N	N	4	4
US-08-637-654-4	US-08-897-438-4	US-08-483-577A-4	US-08-474-671-4	US-08-478-373-4	US-08-337-483-4	US-08-478-435-4	US-08-487-890A-4	US-09-134-001C-1841	US-08-961-527-108	US~09-453-702B-212	US-09-193-562D-29	US-09-175-928-17	US-09-252-329-4	US-08-897-340-4	US-08-785-310A-4	US-08-961-527-317	US-09-124-523-66
Sequence 4, Appli	Sequence 1841, Ap	Sequence 108, App	Sequence 212, App	Sequence 29, Appl	Sequence 17, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 317, App	Sequence 66, Appl							

ALIGNMENTS

APPLICATION NUMBER: US/08/557,115
FILING DATE: 26-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 03063-0171US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 188-3700 TELEPHONE: (404) 818-3700 TELEFAX: (404) 818-3799 INFORMATION FOR SEQ ID NO: 2: ZIF: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA: SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
TYPE: nucleic acid OTHER INFORMATION: /note= "Translation start codon" NAME/KEY: misc_feature LOCATION: 99..101 , Application US/08557115 5731151 King, Harulu ... Sathish, Mundayoor Shinnick, Thomas M. NVENTION: Regulator of Contact-Mediated Hemolysin 191 Peachtree Jones & Askew DNA (genomic) Street, 37th Floor

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PCT-US94-05869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9405869 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                     TELEFAX: (404) 688-988
                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER: LEM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 TGATTATTTGCGAGAGCGTGGGCGTTAATATAAAACAAGAACTAATAAACGCTCTCGCAC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (404) 688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 CCGCA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 TGATTATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTTAAAAACGCAATCGAAA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 AATTTATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTAAAGAGGCGAA 93
                                            STRANDEDNESS:
                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                          LENGTH:
                              COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68;
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                                                                                                                                                                                                                                                                                                                                                                                30303-1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                              Atlanta
           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                              Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                               King, C. H. Sathish, Mundayoor Sathish, Mundayoor Shinnick, Thomas M. Shinnick, Thomas M. NVERTION: REGULATOR OF CONTACT-MEDIATED HEMOLYSIN TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Suite 1200, The Candler Building 127 Peachtree Street, N.E.
                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                        (404) 688-9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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87..94
                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                              linear
No
           DNA (genomic)
                                            double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "4/8 match with consensus sequence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "4/6 match with -35 consensus sequence (TTGACA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "5/6 match with -10
                                                                                                                                                                                                                                                                     PCT/US94/05869
                                                                                                                                                                                     33,438
                                                                                                         2
                                                                                                                                                                       1414.611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33.8;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the E. coli
ribosome binding sites (AGGAAAGG)"
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US-08-325-426B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1,
                                   FILING DATE: 16-DEC-1994 INFORMATION FOR SEQ ID NO: 1:
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
SEQUENCE CHARACTERISTICS:
LENGTH: 10718 base pai:
                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: cDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1
TITLE OF INVENTION: (SINGAPORE STRAIN)
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 CCGCA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 TGATTATTTGCGAGAGCGTGGGCGTTAATATAAAACAAGAACTAATAAACGCTCTCGCAC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 CCGCA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 47..52
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 TGATTATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
wes 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 87..94 OTHER INFORMATION: /noi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 99..101
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                    APPLICATION NUMBER: US/08/325,426B FILING DATE: 16-DEC-1994
                                                                                                                                                                                              COUNTRY: USA
ZIP: 22201-4714
                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                CITY: ARLINGTON
                                                                                                                                                                                                                                                               ADDRESSEE: NIXON and VANDERHYE PC STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08325426B
                                                                                                                                                                                                                              VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                  TAN, Yin-Hwee
                                                                                                                                                                                                                                                                                                                                                                                                                                       FU, Jianlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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99..101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                    Eu-Hian
                                                                                                                                                                                                                                                                                                                                                                                                                      Boon-Haun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "4/8 match with the E. coli
consensus sequence for ribosome binding sites
(AGGAPARGG)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "5/6 match with -10 consensus sequence for E. coli promoters (TATAAT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "4/6 match with consensus sequence (TT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.8; DB Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Translation start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence (TTGACA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57;
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US-08-280-690-1
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Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                             TELEX: 380816 CooleyPA INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: MOLECULE TYPE: HYPOTHETICAL: N
                                                                                                                                                                REFERENCE/DOCKET NUMBER: ST.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5070
TELEFAX: 415-857-0663
                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard L
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 GAAAATCGTTGTATCTAGACTTAGGCTGGTTGGCAAGATACTTTTAGCAACATACTCCGA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Dengue Fever Virus Type 1
STRAIN: S275/90
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/280,690 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                         ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCCAAGGACCCATGAAATTGGTGATGGCTTTCATAGCATTCCTAAGATTTCTAGCCAT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACCACTGGACGGATTTTTATGATGTTTTTTTAGAGGCTTTGGTGACCTGCCTAAAAAT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGAAACCGCGTGTCAACTGGTTCACAGTTGGCGAAGAGATTCTCAAAAAGGATTGCTTTC 196
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5583011
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                                                    nucleic acid
EDNESS: double
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                                                                                         3047 base pairs
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                                    unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA sequence corresponding to
the genomic RNA of DEN1-S275/90
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Compositions, Treatments, and
Diadnostics for Schistosomiasis and Related Diseases
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                                                                                                                                                                                                                                          30,092
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                      Version #1.25
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                                                                                                                                               US-08-464-339A-1
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Patent No. 5747280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.0%;
Best Local Similarity 49.3%;
Matches 75; Conservative
                                                                       Matches
                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1:
1240 ATCAGCAGCCTTTTGRAATTGCTCTCAGNTCAAAGCTGTTTGTTACTCAAATTTCCATAA 1181
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14388
FILING DATE: 9 DEC 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1271 BASE PAIRS
                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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LOCATION:
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                                13 ACCAACCGTTCTATGAAAATCGTTGTATCTAGACTTAGGCTGGGTTGGCAAGATACTTTTA 72
                                                                                                                                                                                                                                                                             TELEPHONE: ZUL .
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CITY: ROSELAND
                                                                                           Local
                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                           Similarity
                                                                                                                                                                                                                     NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EE: CARELLA, BYRNE, BAIN, GILFILLAN, SE: CECCHI, STEWART & OLSTEIN 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HASTINGS, ET AL
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147..2489
                                                                       Conservative
                                                                                                                                                                                    LINEAR
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                                                                                                                                                                                                     SINGLE
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Pred. No. 10;
                                                                                         Score 28.6;
Pred. No. 9;
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                                                                       Mismatches
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                                                                                                          DB 1;
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Patent No. Sequence 1, QΥ g

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                US-09-090-793-12/c
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; Sequence 1, Application PC/TUS9414388
; GENERAL INFORMATION:
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Sequence 12, Application US/09090793
                                                                                                                                                                                                                                                                                             Query Match
rocal Similarity
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SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      1240 ATCAGCAGCCTTTTGRAATTGCTCTCAGNTCAAAGCTGTTTGTTACTCAAATTTCCATAA 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                    1180 GCTTCAAACATCTTACTTCCTTCAGGGGTTTTCTGGTTGTTTTATTTTGACTTTTCCCAA 1121
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                                                                                                                   133 ACCTGCCTAAAAATACTACAAAACAAAATGA 162
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                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: Concu.
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STATE: NEW JERSEY
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ADDRESSEE: CECCHI, STEWART & OLSTEIN
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                                                                                  AGCCCAAAAAAAAAAAAAAAGCAYAATTA 1091
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Pred. No. 9;
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GENERAL IMPORMATION:
APPLICANT: Calgene, LLC
TITLE OF INVENTION: Production of polyunsaturated fatty acids by expression
TITLE OF INVENTION: of polyketide-like synthesis genes in plants
FILE REFERENCE: CGNE.131.01US
CURRENT APPLICATION NUMBER: US/09/090,793
CURRENT FILING DATE: 1998-06-04
CURRENT FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patent.pm
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Patent No. 6399373
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR EILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bouqueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RETITLE OF INVENTION: AND POLYMONPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
FILE REFERENCE: GENSET.031A
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/111,909 PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 140
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TYPE: DNA
ORGANISM: Vibrio marinus
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        IOCATION: 93714
OTHER INFORMATION: 5-128-60 :
                                                FEATURE:
NAME/KEY: allele
                                                                                      LOCATION: 90842
OTHER INFORMATION:
                                                                                                                                                                                 NAME/KEY: allele
LOCATION: 88073
                                                                                                                                                                                                                                                              NAME/KEY: allele LOCATION: 72794
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FEATURE
                                                                                                                               NAME/KEY: allele
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Pred. No. 26;
                polymorphic
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LOCATION: 103806
OTHER INFORMATION:
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LOCATION: 97152
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 134362
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OTHER INFORMATION:
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LOCATION: 108471
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OTHER INFORMATION:
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LOCATION: 108149
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LOCATION: 99098
          NAME/KEY: allele
LOCATION: 72771.
                                               NAME/KEY: allele
LOCATION: 160031
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OTHER INFORMATION:
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LOCATION: 150329
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LOCATION: 108308
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LOCATION: 106940
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LOCATION: 99117
OTHER INFORMATION:
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polymorphic
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FEATURE:
PRAME/KEY: allele
PRAME/KEY: 88050..88096
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PRAME/KEY: BROSO..88096
                                                                     FEATURE:
NAME/KEY: allele
LOCATION: 103783..1
OTHER INFORMATION:
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LOCATION:
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LOCATION:
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LOCATION: 88050..88
OTHER INFORMATION:
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                            LOCATION: 106918...
OTHER INFORMATION:
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LOCATION: 99075.
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OTHER INFORMATION:
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LOCATION: 97099.
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NAME/KEY: allele
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OTHER INFORMATION:
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LOCATION: 90819..90865
                                                   NAME/KEY:
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97130..
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97099..
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93690.
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90819.
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99094..99140
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97130..97177
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allele
106918..106966
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ON: polymorphic
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                               5-133-375
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PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 99
LENGTH: 943
TYPE: DNA
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CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENEST.051CP1
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OTHER INFORMATION: polymorphic fragment 5-135-198
                                                                                                                                                                 NAME/KEY: allele
LOCATION: 443
OTHER INFORMATION: 12-386-155 : polymorphic base
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LOCATION: 108127..108177
                                                   NAME/KEY: misc_binding
LOCATION: 444..462
OTHER INFORMATION: 12-386-155.mis2, complement
                                                                                                               NAME/KEY: misc_binding
LOCATION: 423..442
OTHER INFORMATION: 12-386-155.mis1, potential
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LOCATION: 108084..108130
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OTHER INFORMATION: upstream amplification primer
                    LOCATION:
                                       NAME/KEY: primer_bind
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Chumakov, Ilya
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Pred. No. 39;
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US-09-889-718-1
; Sequence 1, Application
; Patent No. 6412816
; GENERAL INFORMATION:
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; TYPE: DNA
; ORGANIZM: Triticum aestivum
US-09-889-718-1
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US-08-224-391-83/c
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Best Local
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CURRENT FILING DATE: 2001-07-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Aventis CropScience GmbH THILE OF INVENTION: Promotor for gene expression in caryopses of plants FILE REFERENCE: 514413-3886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: DE 100 41 861.9 PRIOR FILING DATE: 2000-08-26 PRIOR APPLICATION NUMBER: DE 100 32 379.0
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IOCARION: 669..688
OTHER INFORMATION: downstream amplification
NAME/KEY: misc_binding
LOCATION: 431..455
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NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: C/O William S. Frommer
STREET: 530 Fifth Avenue
                                                                                           APPLICANT: Paoletti, Enzo
APPLICANT: Pincus, Steven
TITLE OF INVENTION: FLAVIV
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                                                                                                                                                                                         Application US/08224391
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                                                                                               FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
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Pred. No. 17
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Pred. No. 9
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US/08/224,391

25,506

454310-2340

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RESULT 12
US-08-484-304-83/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 83,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 840-07: INFORMATION FOR SEQ ID NO:
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/484,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6534 ATATAAGTAAGAGGAGTATTTCCGTAAGAGTCAGTAATATT 6494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/729,800
FILING DATE: 17-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Paoletti, Enzo
APPLICANT: Pincus, Steven E.
TITLE OF INVENTION: FLAVIVIR
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 CTACAAACAAATGATTATTTGCGAGAGCGTGGGCGTTAAT 188
                                                                                                                                                                        COUNTRY: Un
ZIP: 10036
                                                                                                                                                                                       CITY: New York
STATE: New York
COUNTRY: United States of America
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STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Frommer, William S. REGISTRATION NUMBER: 25,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2340
                                                                                                                                                                                                                                                                                 ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William S. Frommer
                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/224,391
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STATE: New York
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Similarity 48.4%;
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                                                                                                                                                                                                                                                             530 Fifth Avenue
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Pred. No. 20
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US-08-184-009-127/c
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Best Local Similarity
Matches 78; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                          COMPUTER EADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/ME-1-0
                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION UNDER: US/08/184,009
FILING DATE: 19-JAN-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
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ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
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ATTORNEY/AGENT INFORMATION:
                                                            TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6534 ATATAAGTAAGAGGAGTATTTCCGTAAGAGTCAGTAATATT 6494
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APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 CTACAAACAAATGATTATTTGCGAGAGCGTGGGCGTTAAT 188
                                      TELEFAX:
                                                                                                       REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45
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                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                                                                                                    NAME:
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                                                                                                                                                 Frommer, William S.
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COX, William I.

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11.8%;

Score 28.2; Pred. No. 20;

DB 1; 83;

Length 7351; Indels

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                                                                                             ; TOPOLOGY: li
; MOLECULE TYPE:
US-08-566-398-39
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Matches 78; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/08566398 Patent No. 5858373
                                Matches
                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                      TELEPHONE: (212) 840-0712
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Paoletti, Enzo
APPLICANT: Gettig, Russell
TITLE OF INVENTION: RECOMBINANT POXVIRUS - FELINE INFECTIOUS
TITLE OF INVENTION: PERITONITIS VIRUS, COMPOSITIONS THEREOF, AND METHODS FOR
TITLE OF INVENTION: MAKING AND USING THEM
NUMBER OF SEQUENCES: 63
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6654 ATAAAGTTTAAATTTTTTATCATACCAGGTGGAAACAATCTTTCATCGTTATATTCTTTT 6595
                                                                                                                                                                                                                                                          NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6534 ATATAAGTAAGAGGAGTATTTCCGTAAGAGTCAGTAATATT 6494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 7351 base pairs
                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 CTACAAACAAATGATTATTTGCGAGAGCGTGGGCGTTAAT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 ACCACTGGACGGATTTTTATGATGTTTTTAGAGGCTTTGGTGACCTGCCTAAAAATA 147
28 AAAATCGTTGTATCTAGACTTAGGCTGGTTGGCAAGATACTTTTAGCAACATACTCCGAA 87
                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 01-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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LENGTH: 7351 ___
TYPE: nucleic acid
sing
                                                                                                                                                           TYPE: nucleic acid
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                                              Local
                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                              l Similarity
78; Conserv
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                                Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                 linear
                                                                                                             DNA (genomic)
                                                                                                                                           single
                                            11.8%;
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                                               Score 28.2;
Pred. No. 2
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Pred. No. 20;
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                              ed. No. 20;
Mismatches
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Best Local Similarity
Matches 78; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 127, Application US/08458356
                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TENGTH: 7351 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6534 ATATAAGTAAGAGGAGTATTTCCGTAAGAGTCAGTAATATT 6494
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                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 454310-2530 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tartaglia, James APPLICANT: Cox, William I.
6534 ATATAAGTAAGAGGAGTATTTCCGTAAGAGTCAGTAATATT 6494
                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 CTACAAACAAATGATTATTTGCGAGAGCGTGGGCGTTAAT 188
                      148 CTACAAACAAAATGATTATTTGCGAGAGCGTGGGCGTTAAT 188
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ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 ACCACTGGACGGATTTTTATGATGTTTTGTTTTAGAGGCCTTTGGTGACCTGCCTAAAAAATA 147
                                                                                                                                                                28 AAAATCGTTGTATCTAGACTTAGGCTGGTTGGCAAGATACTTTTAGCAACATACTCCGAA 87
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                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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nilarity 48.4%;
Conservative
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(212) 840-0712
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Pred. No. 20;
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Search completed: May 12, 2003, 02:38:28 Job time: 164.429 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length DB
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Gapop 10.0 , Gapext 1.0
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB_seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB_seq:*
4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB_seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB_seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB_seq:*
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9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB_seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB_seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB_seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB_seq:*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB_seq:*
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4956

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                           9 US-09-938-842A-4759

9 US-09-764-891-9719

19 US-09-764-891-9718

10 US-09-764-891-9718

10 US-09-925-302-113

9 US-09-938-842A-4228

10 US-09-938-842A-4228

10 US-09-988-1

7 9 US-10-184-644-522

9 US-10-184-644-522

10 US-09-764-877-2137

11 US-09-764-877-2134

11 US-09-988-1

10 US-09-988-363

11 US-09-988-363

11 US-09-988-363

11 US-09-988-363

11 US-09-988-363

11 US-09-948-767-1

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                           Sequence 522, App
Sequence 523, App
Sequence 2137, Ap
Sequence 2134, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 128, Appli
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Sequence 9713, Ap
Sequence 9718, Ap
Sequence 113, App
Sequence 9, Appli
Sequence 4228, Ap
Sequence 17, Appli
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ALIGNMENTS

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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAIN
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIF1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4759
LENGTH: 2000
TYPE: DNA
ORGANISM: ATABLIGOPSIS thallana
US-09-938-842A-4759
RESULT 2
US-09-764-891-9719
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US-09-938-842A-4759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Harper, Jeff
                                                                                                                                    196 AAGAACTAATAAACGCTCTCGCACCCGCAATTATATTTTGTTCT
                                                                                                                                                                                                                    555 TGGTTATAAATATGAAACATTTACATAATTTAGTAAAACGTTCAACTTGATAAAATAA 614
                                                                                                                                                                                                                                                                        136 TGCCTAAAAATACTACAAACAAAATGATTATTTGCGAGAGCGTGGGCGTTAATATAAAAC 195
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GENERAL INFORMATION: Publication No.

Sequence 9719, Application US/09764891 Publication No. US20030077808A1

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RESULT 3 US-09-764-891-9718 (S-09-764-891); Sequence 9718, Application US/09764891; Publication No. US20030077808A1
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US-09-764-891-9719
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SEQ ID NO 9718
LENGTH: 10951
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity 48.9%;
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Best Local
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
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10049 TAATAAAGCTATAGAGATGGGAAACAAGATTCGTGGTTGCCAGGTCTTGGGAACTGAAGGG 10108
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                                                                                  9989 TGGGGGGACAATCCTAAAGTTTTACACACTGTATGATTCTGTTTTTGTAACATTCTTAAA 10048
                                                                                                                                                                  9929 CABACTACTGATACATGTAACAAATTGCATGGACCTCAAGGGAATTATGCTTGGGTGGTT 9988
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                        131 TGACCTGCCTAAAAAATACTACAAACAAAATGATTATTTGCGAGAGCGTGGGCGTTAATAT 190
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                                                                                                                      11 CGACCAACCGTTCTATGAAAATCGTTGTATCTAGACTTAGGCTGGTTGGCAAGATACTTT 70
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Pred. No. 10;
                                                                                                                                                                                                                                                                         Score 33.2;
Pred. No. 10;
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US-09-925-302-113/c;
Sequence 113, Application US/09925302;
Patent No. US20020044941A1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-302-113
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                                                                       US-09-815-923-9
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                                                                                                                                                                                               SOFTWARE: 1
SEQ ID NO 9
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Best Local Similarity
Query Match
Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                    APPLICANT: Gill, Sarjeet S.
APPLICANT: Ross, Linda S.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as
TITLE OF INVENTION: Target Sites for Insecticides
FILE REFERENCE: 023070-093800US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/815,923
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10109 AA 10110
                                                                                       FEATURE: OTHER INFORMATION: neurotransmitter transporter encoded by inebriated OTHER INFORMATION: gene
                                                                                                                                                           TYPE: DNA
                                                                                                                                        ORGANISM: Manduca sexta
                                                                                                                                                                              LENGTH: 4956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1045
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 Conservative
               13.1%;
54.9%;
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Pred. No. 15;
                  Score 31.4;
Pred. No. 25;
 Pred. No. 25;
); Mismatches
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 51;
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48 TAGGCTGGTTGGCAAGATACTTTTAGCAACATACTCCGAAACCACTGGACGGATTTTTAT 107

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                                                          US-09-790-988-1
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LENGTH: 2000
                                                                                                                                     SEQ ID NO 1
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                    Query Match
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  Best Local Similarity
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                                                                                                                                                   PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
                                                                                                                                                                                                                                                                  APPLICANT: SAKAKI, YOSHIYUKI TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS FILE REFERENCE: 081356/0159
                                                                                                                                                                                                                                                                                                                      APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION UNMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
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TYPE: DNA
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                                                                        TYPE: DNA
ORGANISM: Buchnera
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                                                                                                              CENGTH:
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Local Similarity 63.2%;
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13.0%;
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Score 31.2; DB 10;
Pred. No. 2.6e+02;
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Pred. No. 1
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                Length 640681;
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US-10-184-634-522/c

Sequence 522, Application US/10184634
Publication No. US20030068684A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc

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CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 522
LENCTH: 527
TYPE: PRT
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Best Local :
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Publication No. US20030044930A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83745 AATAAGAGATATTACTTCTACTGAGTCTTTAGTTAATAAAAAAATAATGAAA 83796
341 MMCMRYW.BM...
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                                                                                                                                                                                                          521 YAMN.M.GS...GMA..., TATBGA...C.BH.SRD..WA.HDTTSY.DMTCMDYKB... 462
                                   218 ACCCGCAATTATATTTTGTTCTT 240
                                                                                                      158 AATGATTATTTGCGAGAGCGTGGGCGTTAATATAAAACAAGAACTAATAAACGCTCTCGC 217
                                                                                                                                         461 W.BTYH..MB..HDD.YS.YKTN.MRSSHA.BAY.TY..H.SAKAM.N..BTTCMTMKDT
                                                                                                                                                                          38 TATCTAGACTTAGGCTGGGTTGGCAAGATACTTTTAGCAACATACTCCGAAACCACTGGAC
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                                                                                                                                                                                                                                                                                Local Similarity
les 21; Conserv
                                                                    .NH..HC...BCBK.BCDR.T.R.CNKCCDA..TMAM.DC..HN...
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Goddard, Audrey
Godowski, Paul J
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Gurney, Austin L.
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Watanabe, Colin K.
Wood, William I.
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Pred. No. 12;
2; Mismatches 110; Indels
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US-09-764-877-2137
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; ORGANISM: Homo Sapien
US-10-184-634-522
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 522
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Best Local Similarity 10.3%;
Matches 21; Conservative 7:
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SEQ ID NO 2137
LENGTH: 6931
                                                                                                                                                               Matches
                                                                                                                                                                                                     Query Match
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TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC005
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/764,877 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                 Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
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CURRENT FILING DATE: 2002-06-28
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TYPE: PRT
2903 TCTGAGGCACCTTAGCAACAATTATTATGAAAATTGTCAACAGCGTGTCTTCATGCTTA 2962
                                                                               2843 GTGTTAAGTAAAAGATTAAAAATGCACTGATGAAGCATGGGTTGAAACTTCTCAATATAG 2902
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                                                                                                                                                             Local Similarity hes 74; Conserv
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                                   ACTCCGAAACCACTGGACGGATTTTTATGATGTTTGTTTTAGAGGCTTTGGTGACCTGCC 139
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K.
Wood, William I.
                                                                                                                                                               Conservative
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Pred. No. 12;
2; Mismatches 110; Indels
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Pred. No. 45;
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US-09-790-988-1/c
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US-09-764-877-2134
                                      DD 609177 CTTATCAAGATTTAAAAATCATTTTAGAAAAATAAAAAATATTCACTTAAGGGATCTAT 609118
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LENGTH: 15287
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Best Local Similarity
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SOFTWARE: PatentIn Ver. 2.0
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC005
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDENI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL
FILE REFERENCE: 081356/0159
                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Vei
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP2000-107160 PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                              TYPE: DNA ORGANISM: Buchnera
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                                                                          46 CTTAGGCTGGTTGGCAAGATACTTTTAGCAACATACTCCGAAACCACTGGACGGATTTTT 105
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ATGATGTTTGTTTTAGAGGCTTTGGTGACCTGCCTAAAAATACTACAAAACAAATGATTA 165
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Pred. No. 3.3e+02;
0; Mismatches 57;
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Pred. No. 65;
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NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database; SEQ ID NO 363
LENGTH: 602
TYPE: DNA
CRGANISM: Homo sapiens
US-09-998-598-363
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US-09-464-767-1/c
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                                                                                                                                          Query Match 12.5%;
Best Local Similarity 59.3%;
Matches 51; Conservative
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APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Both, Gerald
APPLICANT: Boyle, David
APPLICANT: Vrati, Sudhanshu
TITLE OF INVENTION: DNA Encoding Ovine Adenovirus (OAV287) and Its Use as a Viral Vec
FILE REFERENCE: 50179-073
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/464,767
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 3
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                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0
                                                               12259 GTTTTATCTACCATTAATCTGGCTAGAAAGCTATTACTGTTAAAAAATTCTGAAACATTG 12200
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Local Similarity 54.8%;
hes 57; Conservative
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94 GGACGGATTTTTATGATGTTTTGTTTT 119
                                                                                                    34 GTTGTATCTAGACTTAGGCTGGTTGGCAAGATACTTTTAGCAACATACTCCGAAACCACT 93
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Pred. No. 1.5e+02;
^. wismatches 35;
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Pred. No. 25;
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; TYPE: DNA; ORGANISM: synthetic construct US-09-464-767-3
Search completed: May 12, 2003, 04:47:58
Job time : 530.571 secs
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APPLICANT: Vrati, Sudhanshu
APPLICANT: Vrati, Sudhanshu
TITLE OF INVENTION: DNA Encoding Ovine Adenovirus (OAV287) and Its Use as a Viri
FILE REFERENCE: 50179-073
CURRENT APPLICATION NUMBER: US/09/464,767
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09464767 Patent No. US20020045249Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                            Matches 51;
                                                                                                                                                                                                                                                                                 Query Match 12.5%;
Best Local Similarity 59.3%;
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                                                                                       12198 GGGCAATTTGTTTTTATAAAAGTTTT 12173
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                                                                                                                           94 GGACGGATTTTTATGATGTTTGTTTT 119
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Pred. No. 1.6e+02;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                        Score
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length: 2000000000
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1326.722 Million cell updates/sec
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AQ343444 |
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AZ370732 :
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ALIGNMENTS

RESULT 1 BH210086 LOCUS VERSION KEYWORDS SOURCE REFERENCE ACCESSION DEFINITION COMMENT TITLE ORGANISM AUTHORS sequence. BH210086 use of end sequences from Schistosoma mansoni (Puerto Rico strain)
sml BAC library for gene discovery and map construction
unpublished (2001)
Other_GSS: Sml-56720.TR
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeiddia; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 687) BH210086 687 bp DNA linear GSS 24-OCT-2001 Sm1-56J20.TF Sm1 Schistosoma mansoni genomic clone Sm1-56J20, DNA GSS. Seq primer: M13 For Class: BAC ends. 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: nelsayed@tigr.org Shetty, J., Simpson, A., Malek, J., Koo, H., LoVerde, P.T. and El-Sayed Schistosoma mansoni. BH210086.1 N.M. Lo.edu), GI:16389299

FEATURES

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Query Match
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46; Conserv
                                                                                                                                                                                                                                                                               Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
Other_GSSs: RPCIII-124DI3.TU
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 600)
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RPCI11-124D13.TV RPCI-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence.
                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBeloBAC11; Site_1: Hin dIII; Constructed in the laboratory of Dr. Denis Le Paslier at the Fondation Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma mansoni agarose embedded DNA was partially digested with Hin dIII. High molecular weight fragments were ligated in pBeloBaC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 7.95 X the haploid genome. Further information can be found in Le Paslier et al. (2000) Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library. Genomics 65: 87-94.*
                                                /organism="Homo sapiens"
/db_xref="qDB:7547316"
/db_xref="taxon:9606"
/clone="RPPCI-11-124D13"
/clone_lib="RPCI-11"
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/clone_lib="Sm1"
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  'cell_type="Lymphocytes'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 TCTATGAAAATCGTTGTATCTAGACTTAGGCTGGCTTGGCAAGATACTTTTAGCAACATAC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 TATATTACACTCTTAATAAGATGATTTAATATTGTAGAAATGTTAATCATTTCAAATTAA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTATACTGCAGAATAAAGGTCTATGTATAGGTTAATCAACCTTAATAAAGAAGTAGAAA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCGAAACCACTGGACGGATTTTTATGATGTTTTTTTTAGAGGCTTTGGTGACCTGCCTA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidoae; Andropogoneae; Sorghum.

1 (bases 1 to 607)

Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                      High
                                                                                                                                                                                                                                                                                                                                                                                                               20. Three-prime sequences, which are obtained with polymmix or T7 sequencing primer, are presented as the reverse complement. Seq primer: JFN PFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: numpratt@uga.edu sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for high quality sequence is below Phred quality 16. The threshold for high quality sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
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                                                                                                                                                                                                                                                                                                                                                                                                        sequencing primer,
Seq primer: JEN RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                       POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An EST database from Sorghum: developing preanthesis pannicles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                  prepared by mass excision."
a 159 c 142 g 164 t
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RPCI11 Human Male BAC Library"
     77 c     95 g     171 t
                                                                                                                /note="Organ: Developing preanthesis pannicles; Vector: pBluescript II SK(-) from Lambda Zap II. Site_1: XhoI; pBluescript II SK(-) from Lambda Zap II. Site_1 in the cloning vector lambda ZaP II. Clones to be sequenced were
                                                                                                                                                                                                               /db_xref="taxon:4558"
/clone_lib="Immature pannicle 1 (IP1)"
                                                                                                                                                                                                                                                                /organism="Sorghum bicolor"
/cultivar="BTx623"
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                 .607
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Score 36.8;
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EST 31-JUL-2001

bicolor cDNA,

USA

SOURCE ORGANISM

KEYWORDS

VERSION ACCESSION DEFINITION AQ343444 RESULT 2

REFERENCE

AUTHORS

TITLE JOURNAL

FEATURES

607;

BASE COUNT ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 ATCATCACCAAGTGAT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 CTACAAACAAAATGAT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  521 AAAATTCTTGTATGTGGGCCTTAGGGCGCCTTTACCTTACCATTTGGGCCATTACGACCAGA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 ACCACTGGACGGATTTTTATGATGTTTTTTAGAGGCTTTGGTGACCTGCCTAAAAATA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 AAAATCGTTGTATCTAGACTTAGGCTGGTTGGCAAGATACTTTTAGCAACATACTCCGAA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCAAGAGGACGGCCTCTCTTACGCTTGGTTACCAAAGTTTGGTTACCCGAGTAAAGCTC 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 012 row E column: 12
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Utah (University of Utah Rm. 308, Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ370732 688 bp DNA linear GSS 02-OCT-200 1M0122E12F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0122E12 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse whole genome
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and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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1 (bases 1 to 688)
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801 585 7177
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                              was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                  polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                       /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0122E12"
                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
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87 AACCACTGGACGGATTTTTATGATGTTTGTTTTAGAGGCTTTGGTGACCTGCCTAAAAAT 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCAGATGACAACGCCAATGATTATT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTACAAACAAATGATTATTTGCGAGAGCGTGGGCGTTAATATAAAACAAGAACTAATA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCCACAGGGATGCTTGGTTTAGTGGTTTTTTAAAAGGCTACTTTGAACAACATAAAATC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila for BDGP is constructing a physical map of the Drosophila for management of the BDGP is constructing a physical map of the Drosophila for BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR36B11 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL074301.1 GI:4954182
GSS:
                                                                                                                                                                                                                                                                                                                                                           melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUN-1999) Genoscope - Centre National de Sequencaç BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                                   and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 1099)
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/organism="Drosophila m
/db_xref="taxon:7227"
/clone="BACR36B11"
/clone_lib="RPCI-98"
/note="end : T7"
a 150 c 135 g :
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a 128 c 119 g 192 t
                                                                                                                                                                                                           .1099
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enoscope.cns.fr
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Mismatches

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   64;
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Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Pukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM161288 EST563811 PyBS Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parasite Genomics Group
The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Jane Carlton
                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: ADF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.malaria.mr4.org/mr4pages/index.html
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   Conservative
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//dev_stage="Reserval blood stages"
//dev_stage="Reserval blood stages"
//lab_host="E. coli XI-1 Blue"
//lab_host="E. col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carlton@tigr.org
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                                                                                                                                                                                          After packaging, the phagemid vector (pAD-GAI4) was excised from the HybriZAP vector and plasmid DNA isolated."
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/strain="17%L"
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BJ437738.1
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BV437738 Dictyostelium discoideum cDNA librarry, VF Dictyostelium
discoideum cDNA clone ddv35a08 3', mRNA sequence.
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Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 696)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the vegetative
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BJ439775 Dictyostelium discoideum cDNA library, VF Dictyostelium
discoideum cDNA clone ddv4lf17 3', mRNA sequence.
                          Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
1 (bases 1 to 483)
Urushihara, H., Tanaka, Y., Kohara, Y., and Shin-i, T.
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Dictyostelium discoideum
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Center For Genetic Resource Information
Center For Genetic Genetics
Contact Institute of Genetics
Conta
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81-559-81-6856
81-559-81-6855
length cDNA of Dictyostelium discoideum at the vegetative
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/strain="AX4"
/db_xxef="haxon:44689"
/clone="ddv41f17"
/clone_lib="Dictyostelium discoideum
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113 c 99 g 263 t
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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BJ383574 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc53bl6 3', mRNA sequence.
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Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
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Location/Qualifiers
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1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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/Strain="AXX4"
/db_xref="taxon:44689"
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/clone="ddv5a08"
                                                                                                                                         /dev_stage="Culmination stage"
106 c 95 g 254 t
                                                                                                                                                                                                               /organism="Dictyostelium discoideum"
/Strain="AX4"
/Strain="AX4"
/db_xref="Taxon.44689"
/clone="ddc53b16"
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79 c 71 g 179 t
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160 AAGAAGACCT 169
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                                                                                                                                                                              GAAAGAACTTTTAAAAATTTTGTGATAATATTTTATAGACTTTTGAAAAAATCGGAAGA 99
                                                                                        1 (bases 1 to 661)
Cariton,J.M.-R. and Dame,J.B.
The Plansmodium vivax and P. berghei gene sequence tag projects
Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
Contact: Dame JB
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611,
Tel: 352 392 4700
Fax: 352 392 9704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS.
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254PbH05 Pb MBN #21 Plasmodium berghei genomic 3', DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: damej@mail.vetmed.ufl.
Seq primer: M13(-20) forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dept. of Pathobiology, College of Veterinary Medicine
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                                                                                                                                                                                                                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                             /note="Wector: And Musically SK(+) vector DNA, phagemid excised from lambda ZAP, Site_1: EcoRV; Site_2: EcoRV; Genomic DNA was prepared from asynchronous blood stage forms of the cloned ANKA isolate of P. berghei grown in laboratory Swiss white mice. The DNA was purified from contaminating host DNA by Hoechast Dye 33258-CSC1 ultracentrifugation and precipitated. Purified DNA was digested with mung bean nuclease in the presence of 36-38% formamide at 50 C, as described (Vernick, E.D., Imberski, R.B., and McCutchan, T.F. 1988. Nucleic Acids Research 16:6883-6896). The ends of the digestion fragments were polished using T4 DNA polymerase, and the fragments size selected in the range 500-2000 bp. These were ligated into the EcoRV-cleaved and dephosphorylated pBluescript SK(+) vector. Recombinant plasmids were used to transform E. coli XII.0-Gold host cells."

23 a 51 c 98 g 188 t 1 others
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/lab_host="Mus musculus"
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/strain="ANKA clone 15cy1 (clone of
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Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                    BJ356150 772 bp
BJ356150 Dictyostelium discoideum discoideum cDNA clone dda59111 3',
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Unpublished (2002)
Contact: Genoscope
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BJ356150.1 GI:19255745
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Location/Qualifiers
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                                                                                                                                                      Urushihara,H., Tanaka,Y., Kohara,Y
Full length cDNA of Dictyostelium
                                                                                                                                                                                                                  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 772)
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/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="inner ear"
/dev_stage="embryonic"
/note="subtracted cDNA library"
/note="subtracted cDNA 11brary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Danio rerio embryonic
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BJ444759 Dictyostelium discoideum cDNA library, V
discoideum cDNA clone ddv57j09 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 541) Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-1, T. Full length cDNA of Dictyostelium discoideum at the vegetative
                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium discoideum.
Dictyostelium discoideum
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                                                                                                                                                                                                                                                     National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
                                                                                                                                                                                                                                                                                                Center For Genetic Resource Information
                                                                                                                                                                                                                                                                                                              Contact: Tadasu
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Mycetozoa; Dictyosteliida;
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               Similarity
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/strain="AX4"
/db_xref="taxon:44689"
/clone="dda59111"
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/dev_stage="Growth phase"
85 c 81 g 212 t
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125 c 158 g 224 t
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Pred. No. 73;
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125 CTTTGGTGACCTGCCTAAAAATACTACAAAACAAAATGATTATTTGCGAGAGCGTGGGCGT 184

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Unpublished (2002)
Contact: Tadasu Shin-i
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                 Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T. Full length cDNA of Dictyostelium discoideum at the vegetative
                                                                                                                     Dictyostelium discoideum
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Fax: 81-559-81-6855
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1 (bases 1 to 594)
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1 (bases 1 to 549)
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89 c 81 g 219 t
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/strain="Ax4"
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/clone_lib="fictyostelium discoideum cDNA library, VF"
/sex="mat A"
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TITLE	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	SCMRPTAA	RESULT 1
Highly repeated short DNA sequences in the genome of Schistosoma mansoni recognized by a species-specific probe	1 (bases 1 to 121)	<pre>Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.</pre>	Schistosoma mansoni	S.mansoni (strain Egyptian) DNA, clone pSm1-7.		M61098.1 GI:161064	M61098	S.mansoni tandem repeat units.	SCMRPTAA 121 bp DNA linear INV 26-APR-1993		

Pred. No. is the number of results predicted by chance to have a

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TITLE
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MEDLINE
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.melanogaster myosin heavy chain gene, 5' J02788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Draft entry and computer-readable copy of sequence provided by S.I.Bernstein, 23-JUN-1987.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and intron locations are conserved compared other organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wassenberg, D.R. II, Kronert, W.A., O'Donnell, P.T. and Bernstein, S.I. Analysis of the 5' end of the Drosophila muscle myosin heavy chain gene. Alternatively spliced transcripts initiate at a single site and intron locations are conserved compared to myosin genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 4676)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myosin; myosin heavy chain.
D.melanogaster (Canton S) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J02788.1
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91187067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
456...>4676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chem. 262 (22), 10741-10747 (1987)
                               /translation="MPKPVANQEDEDPTPTLFVSLEQRRIDQSKPYDSKKSCWIPDRE
EGYLLGEIKARTKGDIVSVGLQGGKTRDLKKDLLQOVNPPKYEKAEDKANLTYTLANDASV
LHALLAGRYYKLLIYTYSGLECVJA.INYKRTYPYTMKCAKNYGXGKRNEUPDHTPAJSD
GALYDMLTNHVNQSMLITGESGAGKTENTKKVIAYFATVGASKKTDEAAKSKGSMEDQ
                   VVQTNPVLEAFGNAKTVRNDNSSRFGKFIRIHFGPTGKLAGADIET
                                                                                                                                                                                                    VVQTNPVLEAFGNAKTVRNDNSSRFGKFIRIHFGPTGKLAGADIET"
join(2381..2584,3144..3287,4138..4518,4592.
                                                                                                                                                                                                                                 /translation="mpkpvanQededptpylfvsleQrridQskpydskkscwipdre

EGYLLGEIKATKGDIVSVGLQGGKVRDIKFEKVEKVNPPKFEKIEDMADMTVLNIPCV

LHNLRQRYYALLITYTSGLFCVAINPYKRFPYTNRCAKMYRGKRRNEVPHIFAISD

GAYVDMLTNHVNQSMLITGESGAGKTENTKKYJAYFATVGASKKIDAAKSKGSMEDQ
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20 c 26 g
                                                                                                       /protein_id="AAA28707.1"
/db_xref="GI:552101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MHC mRNA"
172. .2283
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                                                                                                                                                codon_start=1
                                                                                                                                                               'note="myosin heavy-chain a"
                                                                                                                                                                                                                                                                                                               'db_xref="GI:552100"
                                                                                                                                                                                                                                                                                                                                   'protein_
                                                                                                                                                                                                                                                                                                                                                                  'note="myosin heavy-chain"
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                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                          note="MHC intron A"
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Pred. No.
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REFERENCE
AUTHORS
TITLE
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LOCUS
DEFINITION
ACCESSION
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                                                                                                     Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2263)

George, E. I., Ober, M. B. and Emerson, C. P. Jr.

Functional domains of the Drosophila melanogaster muscle myosin heavy-chain gene are encoded by alternatively spliced exons mol. Cell. Biol. 9 (7), 2957-2974 (1989)
                                                                                                                                                                                                                                        M61229 M27194
M61229.1 GI:157890
myosin heavy chain.
                                                                                                                                                                                                                D.melanogaster (strain Canton
Drosophila melanogaster
                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda;
                                                                                                                                                                                                                                                                                 D.melanogaster myosin
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/note="MHC intron F"

1582 a 984 c 869 g

p upstream of XbaI site.
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2979. 3143
         /strain="Canton S"
/db_xref="taxon:7227"
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<2835. .2978
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/map="chromosome 36B(2L)"
                                      /organism="Drosophila melanogaster"
                                                              Location/Qualifiers
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Note="myosin heavy-chain
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288. .4137
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90.0%;
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heavy chain
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                                                                                                                                                                                                                                                                                 linear
complete cds
                                                                                                                                                                                                    Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4676;
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CDS	CDS	gene	exon	exon
COGOD. STAIT-1 /PCOGUCT="MayS II heavy chain" /PCOCHT. STAIP 157982" /PCOCHT. STAIP 157982	Join(23802583,31463289,41444524,45974660, 47294827,50295132,81428549,93739543,1053811127, 1329913416,1412214385,1590216111,1633317219, 1780817886,1822319398,1946620371,2157821661) /gene="MHC" /note="late-pupal stage myosin heavy chain"	"Mumber"-2 join(23802583,31463289,41444524,45974660, 47294827,69687077,81428549,93739543,1053811127, 1207812195,1412214385,1590216111,1633317219, 1739117469,1822319398,1946620371,2157821661)	/number=1 22832583 /gene="MHC"	456471 /gene="MHC"
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            Unpublished (1998)

2 (bases 1 to 68379)

Celniker.S.E., George.R.A., Galle,R., Svirskas,R.R., Hoskins,R.A.,

Celniker.S.E., George.R.A., Galle,R., Svirskas,R.R., Hoskins,R.A.,

Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Chavez,C.,

Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A.,

Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A.,

Hummasti,S.R., Karra,K., Kearney,L., Kim,S.H., Lee,B.,

Lomottan,M.A., Mak,J., Mazda,P., Mok,M.S., Moshrefi,R.,

Donoth, F.
                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophildae; Drosophila.

1 (bases 1 to 68379)
                                                                                                                                                                                 Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Richards, S., Sequeira, A., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Zieran, J.L. and Rubin, G.M.

Zieran, J.L. and Rubin, G.M.

Sequencing of Drosophila chromosome 2L, region 36B1-36B2
                                                                                                                                                                                                                                                                                                                  Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K.,
  Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Punch,E.
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DS06436, complete sequence.
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/gene="MHC"
22304. .22309
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/gene="MHC"
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21753. .21758
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17808.
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'gene="MHC"
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'gene="MHC"
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'gene="MHC"
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                                                                                                                                                                                                                                                                                              Direct Submission Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA This sequence was identified as CDM:10210880 by the submitter For more information on this record e-mail to fly@celera.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
Drosophila melanogaster.
Drosophila melanogaster.
Eukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota;
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-JUN-1998) Drosophila Genome Center, Laboratory, MS 64-121, Berkeley, CA 94720, USA
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Zieran,L.L. and Kimmel,B.E.
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                                                                                                             /organism="Drosophila melanogaster"
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16461 c 15838 g 23698 t
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/strain="y; cn bw sp"
/db_xref="taxon;7227"
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Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K. Y. Busam, D.A.,

Carlson, J. W., Center, A., Champe, M., Davenport, L.B., Dietz, S. M.,

Dodson, K., Dorsett, V., Doup, L. E., Doyle, C., Dresnek, D., Farfan, D.,

Perriera, S., Frise, E., Galle, R. F., Garg, N. S., George, R. A.,

Gonzalez, M., Houck, J., Hoskins, R. A., Hostin, D., Howland, T. J.,

Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,

McIntosh, T. C., Moy, M., Murphy, B., Nelson, C., Nelson, K. A., Nunoo, J.,

Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,

Phouanenavong, S., Pittman, G. S., Puri, V., Richards, S., Scheeler, F.,

Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S. M.,

Sequencing of Drosophila Chromosome 2L, region 36A-36B

uppublished

J. Marses 1 + 175.132
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Rogers, Y., An, H., Baldwin, D., Banzon, J., Besson, K.Y., Busam, D.A.,
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Pacleb, J., Paragas, V., Park, S., Partel, S., Pfeiffer, B.,
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Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Daveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ш
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Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 175413)
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BACR26003, complete seque
                                                                                                                                                                                                                                                                                                                            This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berkeley, CA 94720,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-AUG-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron R
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/clone="BACR26003 (D1298)"
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
                                                                                                                                                                     /strain="y; cn bw sp"
/db_xref="taxon:7227"
                                                                                                       /map="36A-36B"
                                                                                                                                      'chromosome="2L"
                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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36A-36B, BAC clone
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                                                                                                                                                                                                                                                         ANDIEWS-FLAINCOLL, BASILWALL, BASILEW, A. BASEN, A. BOTKOVA, D. BOTKONA, D. BOTKONA, D. BOTKOVA, D. BOTKONA, D. BOTKOVA, D. BOTKOVA, D. BOTKOVA, D. BOTKOVA, D. BOTKONA, D. BOTKOVA, D. BOTKOVA,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
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Pred. No. 2
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                                                                                        Gibbs, R.A., Rubin, G.M. and Venter, C.J.
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36055 section 45
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FEATURES
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                                                                                                                                                                                                       WERRAQDGDFLLQLQDAETGHGFLNTYKGTELQTECLQLRRASSYQFRLRSENEAGFS
PWSPEVSYRTLAERPGRPGKPHAKGKIHGTQFKARWDAPSDSGGAEILCYHLELSAAG
PAYERIYSGAETEAWCERLQPGTYYALKACCEGPAGQSPYSDIGHYTTEAYPPSAPPP
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KKLKKLEKQRESNPPHSPSPRANELNGHNUNI PPGVPLPGHLHUHHHAVNHGRR
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EEYHHENSI I EQLSALEKPEVLDVTSRAAK I I WESPALANTVTVDMRQLEVGVLLCDS
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QEGSVCLMELPGQLGMQLTLEWQHSKNSFNDRVEYELQYAVLGAAELEGESLSPKGRS
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AGHNYIKLKWGENGNGKVVNSNPSGNGGDFTKYFVEMYVARAKQFQAVYSGTNCMCKV
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QHQHHMHHSHHMHHAHHPHTGMGGSSSNSSSSTAAAISSSLAQAGGLKRIVCKVTSLY
SNRRRLSDQQKAVCIVVSFLVGTFLVAMLVNMLRG"
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GGISGATDSHHQHQHHMHSHHMHAHHPHTGMGGSSNSSSTAALSSSIAQAGGI
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PSELDPSSATCHHHLHGSTATPAMASSQRSSRKLSAGNGSTNGLEMRSVSASAISGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSINLRWAAPAANGASIQHYLLEYDEGRMPGQPQKFVELAKIKAKHYVIGKLQPTTYY
SFRLAAVNEAGQSPYSPVASYSTSGNPPPVPKPPQLLASSSSSLKLGWERRAQDGDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPPPQQQQQQPPQQPAPQGPPPPQQQQQQQQQQVAPPAVQGAPSTGSVGAAQGAPA
TATATHTHAHSHSHSHAHSHTHPQPHAHSPHSPSPPNYRDERSQRQHNKLLRKLEKQR
ESNPPHSPSPRRANELNGHNNNNTPFGVPLPGHLNNHHHAVNHQGRRLPQQHQGQAHQ
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/prod:----
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QISAIEKPEVIDVTSRAAKIIWESPAIANTVTVDMRQLRYQVLLCDSGKQCKYKSLYQ
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                                                                                                                                                                                                                                                                                                                                                                           HKLQERSSYTFRIYAHTDRAGDGDYSEEFVFETSATLPANIKPPRVVQEGSYCLMELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEAYECTVQDLQPGQDYLVRLQVHYQKLTGTVSDPTEFRTPPCEPDQPPPPKLVSRTK
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Query Match 84.0%; Score 16.8; DB 3; Length 258166; Best Local Similarity 90.0%; Pred. No. 2.6e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps

0;

RESULT 8 AC095629

4ب

REFERENCE

AUTHORS

KEYWORDS VERSION ACCESSION DEFINITION

ORGANISM

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Db 153544 GAACTGAATCCGACAAACCG 153563
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                                                                                                                                                                 Worley,K.C.
Direct Submission
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, of Molecular and Human Genetics, Daylor College of Medicine, TX 77030, USA
Direct Submission
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hale, S., Ha
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muzny, D.M.,
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, *** SEQUENCING IN PROGRESS ***,
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COMMENT
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On Jul 10, 2002 this sequence version replaced gi:17942183
                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/doocs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
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Consensus quality: 43940 bases at least Q30
Consensus quality: 47263 bases at least Q30
Consensus quality: 50225 bases at least Q20
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Center clone name: CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                            http://genemark.biology.gatech.edu/GeneMark/), Fgenesh
(http://www.softberry.com/), and GeneSplicer (Mihaela Pertea and
Steven Salzberg, contact mpertea@tigr.org), searches of the
complete sequence against a peptide database and the plant EST
database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated
genes are named to indicate the level of evidence for their
annotation. Genes with similarity to other proteins are named after
the database hits. Genes without significant peptide similarity but
with EST similarity are named as unknown proteins. Genes without
protein or EST similarity, that are predicted by more than two gene
prediction programs over most of their length are annotated as
htppothetical proteins. Genes encoding trNAs are predicted by
tRNAscan-ES (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
Simple repeats are identified by repeatmasker (Arian Smit,
http://ftp.genome.washington.edu/RN/RepeatMasker.html).

1. 13227

11. 13227
                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (29-AUG-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, rbuelletigr.org
On Mar 31, 2001 this sequence version replaced gi:13310897.
Address all correspondence to:rice@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC079890 132927 bp DNA linear PLN 29-AUG Oryza sativa chromosome 10 BAC OSJNBb0089A17 genomic sequence,
                                                                                                                                                                                                                                                                                                              Genes were identified by a combination of several methods: Gene prediction programs including genscan and Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buell, C.R., Yuan, Q., Ouyang, S., Moffat, K.S., Hill, J.N., Burr, P.C., Hsiao, J., Zismann, V., Pai, G., Bowman, C.L., Fujii, C.Y., Yanaken, S.E., Bowman, C.L., Craven, B., Utterback, T.R., Khalak, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org [bases 1 to 132927)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (31-MAR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
4 (bases 1 to 132927)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (16-SEP-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
3 (bases 1 to 132927)
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Buell, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete sequence.
AC079890
                                                                                                                                                                                                                                                                                                                                                                              BAC clone OSJNBb0089A17 is from Oryza sativa chromosome 10 The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org 6 (bases 1 to 132927)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buell, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa chromosome 10 BAC OSJNBb0089A17 genomic sequence
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1 (bases 1 to 132927)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feldblyum, T.V., Quackenbush, J., White, O., Salzberg, S.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC079890.13 GI:13491223
/organism="Oryza sativa"
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BASE COUNT ORIGIN

Query Match Best Local Matches

TocaT N

FEATURES

source

RESULT 9 AC079890

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83403

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mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AT_rich" complement(13435. .13464\/rpt_family="AT_rich")
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Complement (17572. .17613)
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complement (17622. .17642)
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complement(15414.
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complement(15206. .15247)
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SADDVAPCVVHADADEQPAAAAKNDDDDGSTTAPVAAAAAAAAAAAADEQQLFDLFDLLFD
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from this gene"
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                                                                                        /gene="OSJNBb0089A17.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQDGPFGFPAMWAPLADVDEVNAELRLEEPLLWDLGVTDA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map="near C797"
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5. .11237
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                                              VERSION
KEYWORDS
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                                                                                                                                                 AC092272/c
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                          SOURCE
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                                                                                                                                  LOCUS
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Best Local
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    ORGANISM
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                                                                                                                                                                                                                                                                                                                                             Local Similarity
    Homo sapiens
                                                                                                                                  AC092272
                      Homo sapiens.
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2 ATCTGAATCCGACCAACC 19
                                                                                                                                                                                                                                              ATCTGAATCTGACCAACC 105056
HTG.
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to quinone oxidoreductase GB:AAA23691 GI:145766 (Escherichia coli)" join(<29995. .30039,30157. .30295,31110. .31336,31482.
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DDDDAEAAAFLPRDVLDALDGTPPPPPPMYHGVSUYHHAVMAPMLPPPPWAELNPM
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YGPCVESVMVEKAAAGQLPVYGRVVLRCPSMIPVVLDGQQTAKYMIKGRHLMARIYVP
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LLFSMDGDFAPLPELVKLRRKYGFLLVIDDAHGTLVCGENGGGAPELFECENEIDISV
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KAAEEYGMGPRGSALICGYTTYHKNVEESLAELKKKEDCLLCPTGFSANMAVMTALGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="OSJNBb0089A17.10"
                                                                                                                                                                                                                                                                                                                                                                      82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _family="(CGG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _family="(CGG)n"
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                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                         Score 16.4;
Pred. No. 4.
                                                                                                          145668 bp
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                                                                                                             linear
                                                                                                             PRI 24-OCT-2001
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COMMENT

TITLE

TITLE

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REFERENCE
AUTHORS
TITLE
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AC019350/c
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KEYWORDS
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                   Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Bailwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Cheepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gaep, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Loke, K., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Handers, T., Liehoczky, J., Levine, R., Lieu, C., Liu, G., Looke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McDheeters, R., Meldrim, J., Meneus, L., Morroy, J., Naylor, J., McDheeters, R., Meldrim, J., Meneus, L., Morroy, J., Naylor, J., McCheefers, R., Meldrim, J., McDheeters, R., McKernan, K., McKernan
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Drive, Walnut Creek, CA 94598, USA
On Oct 24, 2001 this sequence version replaced gi:14589461.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-JUL-2001) Production Sequencing Genome Institute, 2800 Mitchell Drive, Walnut 3 (bases 1 to 145668)
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17; Conser
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-276018
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Norman, C.H., O'Connor, T., O'Donnell, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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Location/Qualifiers
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/chromosome="5"
/clone="CTC-339E17"
_28057 c 27632 g 42189
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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94.4%; Pred. No. 4.3e+02;
tive 0; Mismatches 1;
Meneus,L., Morrow,J., Naylor,J
O'Donnell,P., Olivar,T.M., Pete
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SOURCE

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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatWasker.html
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All repeats were identified using RepeatMasker:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15065 15164: gap of 100 bp
15165 22791: contig of 7617 bp in length
22782 22881: gap of 100 bp
22882 39817: contig of 16936 bp in length
39818 39917: gap of 100 bp
39918 39917: gap of 18925 bp in length
58843 58942: gap of 100 bp
58843 102439: contig of 43497 bp in length
58843 102439: contig of 43497 bp
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Insert size: 155013; sum-of-contigs
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102540 155813: contig of 53274
Location/Qualifiers
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2536 2635: gap of 100 bp
2636 5535: contig of 2900 bp in length
5536 5635: gap of 100 bp
5536 9094: contig of 3459 bp in length
9095 9194: gap of 100 bp
9095 9194: gap of 100 bp
9195 15064: contig of 5870 bp in length
                                                                                                                                                                                                                                         /note="assembly_fragment"
2636. .5535
                                                             vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-276018"
'note="assembly_fragment"
                                                                                                                                      note="assembly_fragment/
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                  37737 GATCTGAATCCTACCAAC 37754
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559 GATCTGAATCCTACCAAC 1542
                                               1 GATCTGAATCCGACCAAC 18
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                                                                            l Similarity
17; Conserv
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AC091914
                                                                                                                                                                                                                                                                                                                                                            Submitted (27-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 27, 2002 this sequence version replaced gi:14579738.
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (09-JUN-2001) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 3 (bases 1 to 16537)
DOE Joint Genome Institute and Stanford Human Genome Cer
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                    Quality: Phrap Quality >=40 99.5% of Sequence; Estimated Total Number of Errors is 0.5.
                                                                                                                                                                                                                                                                                                   Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 165237)
DOE Joint Genome Institute.
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                                                                            Conservative
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/note="assembly_fragment"
4 30751 c 29180 g 43159
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                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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22882 39817
                                                                                                                                                     /clone="RP11-221N1"
30135 c 32136 g 56114
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39918. .:58842
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                                                                                                                                                                                                                                      .16523
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                                                                                           82.0%;
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94.4%;
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                                                                                           Score 16.4; DB 9;
Pred. No. 4.3e+02;
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Pred. No. 4.3e+02;
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                                                                                                        Length 165237;
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94598, USA
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VERSION
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AC114308
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                                                                                                                                                                                                                                                                             source
1 GATCTGAATCCGACCAAC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 171433 bases at least Q40
Consensus quality: 17924 bases at least Q30
Consensus quality: 179324 bases at least Q30
Consensus quality: 179435 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 175000; agarose-fp estimation
Quality coverage: 9.88 in Q20 bases; agarose-fp estimation
Quality coverage: 9.77 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draff' sequence. It currently
* consists of 5 contigs. The true order of the places
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
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Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joi
Thatitute, 2800 Mitchell Drive, Walnut Creek, CA 94598,
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AC114308
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Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
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Homo sapiens chromosome 5 clone
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DOE Joint Genome Institute.
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                                                             Similarity
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                                                                                                                                                  54617
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1371
12249
12349
33986
                                          Conservative
                                                                                                                                                  b
                                                                                                                                         /clone="RP11-197F21"
/clone_lib="RPCI human BAC
32530 c 33575 g 56124 t
                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .177246
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                                                                                                                                                                                                                                                                                                               1270: contig of 1270 bp in length
1370: gap of unknown length
12248: contig of 10878 bp in length
12348: gap of unknown length
33985: contig of 21637 bp in length
34085: gap of unknown length
79299: contig of 45214 bp in length
79399: gap of unknown length
177246: contig of 97847 bp in length.
                                                                                                                                                                                                                                                                                                                     177246:
                                                           82.0%;
                                       0;
                                                           Score 16.4; DB 2;
Pred. No. 4.3e+02;
                                            Mismatches
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t 400
                                                                             DB 2;
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                                                                               Length 177246;
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84991 GATCTGAATCCTACCAAC

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AC012160/c
                            REFERENCE
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                                                                                           Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,

Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,

Carlson, X., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,

Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,

Ferriera, S., Frise, E., Galle, R.F., Gargy, N.S., George, R.A.,

Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,

Ibeywam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,

McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,

Pacleb, J., Paragas, Y., Park, S., Patel, S., Pfeiffer, B.,

Phouanenayong, S., Pittman, G.S., Putt, V., Richards, S., Scheeler, F.,

Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,

Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 172069)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For more information on this record e-mail to fly@celera.c
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Drosophila melanogaster, chromosome
BACR05602, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10214038 by the submitter. For more information on this record e-mail to fly@celera.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIG
Celniker, S.E., Agbayani, A., Arcaina, T.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
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AC012160.6 GI:17646875
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                                                 Unpublished (1998)
                                                                      Sequencing of Drosophila chromosome X, region
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16; Conservative
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/db_xref="taxon:7227"
2174 c 1909 g 2539 t
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  Baxter, E., Blazej, R.G.,
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Search completed: May 12, 2003, 01:51:34 Job time: 391 secs

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JOURNAL
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Submitted (21-OCT-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
on Dec 13, 2001 this sequence version replaced gi:6466928.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
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/clone_lib="RPC1-98 (ROSWell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
pBACe3.6)"
a 35590 c 36029 g 51479 t
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="x"
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GFP-Sm1-7 fusion p
DNA encoding a Sta
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ALIGNMENTS

RESULT 1
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ANATOMOLI 1
ANATOMOLI 2
ANATOMOLI Diagnosing infection by parasites of the Schistosoma sp. in a biological sample especially useful in cases of low infection intensity, comprises detecting a specific region of the DNA of 04-APR-2000; 2000BR-0001536. Schistosoma mansoni repeater unit 5' PCR primer. 07-JAN-2002 AAI70401; AAI70401 standard; DNA; 20 WPI; 2001-648561/74. Teles Rabello AL, 04-APR-2001; 2001WO-BR00035 11-OCT-2001. WO200175148-A1. Schistosoma mansoni. Schistosomiasis; infection; diagnosis; PCR primer; ss. (FIOC-) FIOCRUZ FUNDACAO CRUZ OSWALDO. (first entry) Dias Neto E, ΒP Pontes LA;

Streptococcus pneu

Schistosoma by polymerase

chain reaction

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                                                                                                            Diagnosing infection by parasites of the Schistosoma sp. in a biological sample especially useful in cases of low infection intensity, comprises detecting a specific region of the DNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schistosomiasis;
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                                                      Claim 1;
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                                                                                                                                                                                                                                                                                                                 04-APR-2000;
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                                                                                            βğ
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                                                                                                                                                                                                                                                                                                                 2000BR-0001536.
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                                                                                            polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "primer of AAI70401" 91..110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers complement (1..19)
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the DNA of
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The present sequence in

sequence is that of a highly repeated short the genome of Schistosoma mansoni. PCR prim

primers

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RRESULT 3
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multicellular parasite transformed with a transgene. Transgenic eukaryotic parasites are useful as universal grafts for in vivo delivery of beneficial gene product in humans and animals. The parasites can particularly be used for restoration of deficiencies whether acquired or genetic, such as hormone deficiencies, metabolic deficiencies,
                                                                                                                                                                                                                                                                                                                                                                             Eukaryotic diploid multicellular parasite useful as universal grafts for in vivo delivery of beneficial gene products in humans and animals involves transformation with a transgene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         universal graft; transgenic eukaryotic parasite; acquired deficiency; genetic deficiency; hormone deficiency; metabolic deficiency; haematological deficiency; immunological deficiency; immunological deficiency; anti-microbial therapy; anti-cancer therapy; drug addiction; poisoning condition; geriatric condition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFP-Sm1-7 fusion construct; circular; green fluorescent protein; glutathione S-transferase; eukaryotic diploid multicellular para
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFP-Sm1-7 fusion protein construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA46170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          demonstrate little
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2000
                                                                                                                                                                     (GFP) coding sequence from Aequorea victoria, and SM1-7 coding sequence from Schistosoma, along with
                                                                                                                                                                                                                                                           This sequence represents a GFP-Sm1-7 fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hamburger J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUN-2000
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                                                                                                                                          promoter sequences. The invention relates to a eukaryotic diploid
                                                                                                                                                                                                                             recombinant vector. This sequence contains the green fluorescent
                                                                                                                                                                                                                                                                                                                   Example
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                                                                                                                                                                                                                                                                                                                   6; 90pp; English.
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                                                                                                                                                                                                                                                              construct
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Black MT,
Pratt JM,
                                         The present sequence encodes a Staphylococcus aureus protein of unknown function. The present sequence was isolated from a library of clones of S. aureus wCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The encoded protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect that some product is a sequence of the control of bacterial action. These vaccines and antibodies would protect that section the control of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT83836 standard;
  Staphylococcal
                            a host against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutagenesis and malignant transformation.
                                                                                                                                                                                                                                                                                             Claim 9; Page 702; 989pp; English.
                                                                                                                                                                                                                                                                                                                                                 aureus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW27874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxic shock syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                        Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - to isolate antimicrobial compounds, and in vaccines against S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-424969/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GATCTGAATCCGACCAACCG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burnham MK,
Reichard RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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     infection,
                         invasion by S. aureus, and conditions relating to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hodgson JE,
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  e.g.
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, Ward JM;
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1.6;
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1843
                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG195ABL30511), expressed DNA sequences (ABLIG195ABL30511) and the encoded proteins
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specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 37321;
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11-JUL-2000; 2000US-0614150
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pharmaceutical;
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                                                                                                                                                                                  Sequence 22188 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY.
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                                         1 GATCTGAATCCGACCAACCG 20
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GAACTGAATCCGACAAACCG
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                                                                                          Conservative
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                                                                                                                                                                                                                                                      for this patent did not form part of the printed was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                    6664 A; 5376 C; 4559 G; 5589
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                                              Polymorphic marker; allele-specific; probe; amplification; PCR primer; hybridisation; plant; hybrid certification; genetic contribution; progeny; back-cross; hybrid; ancestry; corn; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABB57737-ABB72072)
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interactions -
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11-JUL-2000;
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16; Conserv
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2000US-0614150.
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e invention
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Best Local &
                                                             04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV51401-V51704 are forward PCR primers used to amplify fragments of the Zea mays genome in order to detect polymorphic markers. Such markers can be used in the construction of allele-specific primers and probes for amplification or hybridisation, e.g. to determine common or disparate ancestry between 2 or more plants, to monitor the genetic contribution of an ancestral plant, to trace the progeny of proprietary plants, in certification of a hybrid plant or to identify the progeny of a back-crossed plant with an ancestral plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 8
1862
                                                                                                                                                                                                                                                                                                                                                                                                           Human; brain expressed exon; gene microarray; Alzheimer's disease; mepilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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02-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK11862 standard; DNA;
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(MOLE-) MOLECULAR DYNAMICS INC
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17; Conserv
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                                                                2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                   2000US-0180312.
2000US-0207456.
2000US-0608408.
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960S-0032069
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89.5%;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    e expression analysis; probe;
multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probe
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RESULT 9

AAS55514/C

ID AAS55514; standard; D

XX AAS55514;

AC AAS55514;

XX DT 13-FEB-2002 (first of the continuous preumonous pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn
  The invention relates to antisense inhibitors of prokaryotic cellular proliferation, their use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 530 BP; 151 A; 132 C;
                                                                                                                         New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                  WPI; 2001-611495/70.
P-PSDB; AAU37655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001WO-US09180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibiotic; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4;
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nes 17; Conser
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                                                                                                                                                                                                                                                                                                                                            ELITRA PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
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                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-253625P
                                                                                                                                                                                                                                                                      Ohlsen
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae DNA for cellular proliferation protein
                                                                      ID No 9151; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prokaryotic
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Pred. No. 1
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                                                                                                                                                                                                                                                                                            Wall D,
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                                                                                                                                                                                                                                                                                            Trawick JD,
  genes essential identifying the
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ABQ53190/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one
                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes, their use in the discovery of novel antiblotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide for detecting cytosine methylation SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABQ53190 standard; DNA; 1173
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                                                                                                                                                       Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                              Olek A,
                                                                                                                                                                                                                                                                                                                                01-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2002
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                                                                                                                          Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                              (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     596 ATCTGAATCCGACGAACTG
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                                                                                                                     56pp + Sequence Listing; 56pp;
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2000DE-1044543
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Pred. No. 1.
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Best Local S
Matches 17
This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-Cp0-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplion is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two
                                                                                                                                                                                                                 Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
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                                                                                                                                                                                  Claim 12; 56pp + Sequence Listing; 56pp; German.
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05-SEP-2000; 2000DE-1044543.
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Pred. No. 1.9e+02;
""amatches 2;
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Best Local :
This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligoners, the degree of methylation is calculated. The metho is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide for detecting cytosine methylation
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Best Local
                                                                                                                                          This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug; side effect; cancer; cemuna drug; side effect; cancer; cemuna drug; system; gastrointestinal; respiratory system;
is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                methylation status of many C residues to be determined simultaneously. ABQ13410 ABQ134121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ52081 standard; DNA; 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-371829/40
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56pp + Sequence Listing; 56pp;
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2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for detecting cytosine methylation SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; central nervous system; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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bred. No. 1
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Query Match
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Matches 16

Similarity

77 94.1%; .0%;

Score 15.4; DB Pred. No. 2.4e+C

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Length Indels

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RESULT 14
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Best Local (
                   The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB5300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition are useful for the invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. The present sequence is an oligonuclectide used in an example from the invention.

Note: The sequence data for this patent is based on equivalent patent w0200177334 (published 18-OCT-2001) which is available in electronic format directly from WIFO at ftp. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactococcus lactis IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactococcus lactis oligonucleotide #197 used in Long Range PCR
Sequence 22
                                                                                                                                                                                                                                               lactis
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                                                                                                                                                                                                                                                                                                                     Bolotine A,
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                                                                                                                                                                                                                                                              nucleotide sequence useful in
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17; Conserv
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                                                                                                                                                                                                                                               related species
BP;
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                                                                                                                                                                                                                                                                                                                     Sorokine A,
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7 A; 7 C; 5
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89.5%;
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                                                                                                                                                                                                                                                                                                                     Renault P,
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G; 3 T; 0 other;
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RESULT 15

RESULT 15

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Search completed: May 12, 2003, 01:14:56
Job time: 40.2143 secs
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Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIJ6176-ABIJ6171), expressed DNA sequences (ABIJ18167-ABIJ6171), expressed DNA sequences (ABIJ181737-ABB72072).

(ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000\ \mathrm{or} more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 15262; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-08-455-925-1

US-08-455-925-97

US-08-96-259-22

US-08-176-520A-5

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US-08-461-985-5

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US-08-461-985-5

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SSULT 2 Sequence 5, Sequence 5, GENERAL INF GENERAL INF APPLICANT: TITLE OF I FILE SEFER CURRENT AP CURRENT FI	Best Low Matches Matches 1 7 843	LENGTH: 3 LENGTH: 3 TYPE: DNA ORGANISM: FEATURE: NAME/KEY: LOCATION: OTHER INF 08-932-787	CURRENT F PRIOR APP PRIOR FIL PRIOR APP PRIOR FIL PRIOR APP PRIOR FIL PRIOR FIL PRIOR FIL PRIOR FIL RIOR APP PRIOR FIL RIOR APP PRIOR FIL RIOR APP	SULT 1 Sequence 5, Sequence 5, GENERAL INF APPLICANT: TITLE OF I TITLE REFER CURRENT AP		44444 010840	. 3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5	22 C C C C C C C C C C C C C C C C C C
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cion US/08: et al. A FAMILY 430-Y-1 NUMBER: U	conservative AATCCGACCAACC	(2018) ERK3 C	p 0 0 0 0 7	ion US/08932 et al. et al. ANTIBODIES KINASES 430-A-1 NUMBER: US/		993 1176 1176 1176 1176 1176	41 218 218 218 218	3763 4137 4266 6492 6516 30
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al. al. rewrity of MAP2 PROTEIN KIN 0-Y-1 MBER: US/08/932,012C 1997-09-17	0; Mismatches	Score 15.8; DB 4	18 469,547 178,488 7701,544 532,004 Version	787B DIRECTED TOWARD 08/932,787B	ALIGNMENTS	US-09-109-063-2 US-09-109-063-2 US-08-689-421-18 US-09-389-528-18 US-09-181-827A-18 US-09-181-827A-18	US-09-109-063-17 US-09-035-648-14 US-09-001-951-14 US-08-818-829-14 US-08-908-643C-4	US-08-961-527-186 US-09-221-017B-329 US-09-651-011A-3 US-08-961-527-18 US-08-961-527-105 US-08-961-527-105 US-09-045-244A-3 US-09-0453-16
KINASES	2; Indels 0; Gaps 0;	; Length 3671;		extracellular signal-related		Sequence 20 Sequence 2, Sequence 1, Sequence 18 Sequence 18 Sequence 18	Sequence 11 Sequence 12 Sequence 14 Sequence 14 Sequence 14	Sequence Sequence Sequence Sequence Sequence Sequence

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CURRENT APPLICATION NUMBER: US/08/888,818C
CURRENT FILING DATE: 1997-07-07
PRIOR APPLICATION NUMBER: 08/478,985
PRIOR FILING DATE: 1995-06-07
PRIOR PILING DATE: 1994-01-07
PRIOR PILING DATE: 1994-01-07
PRIOR APPLICATION NUMBER: 07/701,544
PRIOR APPLICATION NUMBER: 07/512,004
PRIOR APPLICATION NUMBER: 07/532,004
PRIOR APPLICATION NUMBER: 07/532,004
PRIOR APPLICATION NUMBER: 07/532,004
PRIOR FILING DATE: 1990-06-01
NUMBER: OF SEQ ID NOS: 21
NUMBER: 0F SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 3.0
                                                      RESULT 4
US-08-948-176-24
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Sequence 24, Application US/08948176 Patent No. 5945585 GENERAL INFORMATION:
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                                                                                                                                                                                                    Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative (
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TYPE: DNA
ORGANISM: RAT
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PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: 08/178,488
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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LOCATION: (303)...(2018)
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LOCATION: (303).
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VENTION: A FAMILY OF MAP2 PROTEIN KINASES

NCE: REG 430-V-1
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RESULT 5
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US-09-221-017B-373/c
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; Patent No. 6444799
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STALL.
COUNTRY: USA
ZIP: 94304-1018
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
Version 2.(
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INFORMATION FOR SEQ ID NO: 2/
SEQUENCE CHARACTERISTICS:
SEQUENCE 1531 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/631,264
FILING DATE: DECRMBER 20, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                             TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1062 GATCTGCATCCACCCAACCG 1081
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OPERATING SYSTEM: MICROSOFT WORD FOR
SOFTWARE: MICROSOFT WORD VERSION 7.0
CURRENT APPLICATION DATA:
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APPLICANT: YADAV, NARRADRA S.
TITLE OF INVENTION: ACVI-ACP THIOESTERASES GENES
TITLE OF INVENTION: AND THEIR USE IN ALTERING PLANT
TITLE OF INVENTION: OIL COMPOSITION
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: CHRISTENBURY, LYNNE M. REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: CR-
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Pred. No. 35;
0; Mismatches
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US-08-435-925C-1
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                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08435925C Patent No. 5646025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
PILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: MONTOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 50-813-5600
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: MOYER, DONNA
TITLE OF INVENTION: SCYTALIDUM CATALASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 7096 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                             4931 TGAATCCGACCAACC 4917
                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/435,925C
APPLICATION NUMBER: US/08/435,925C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PP11:
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 00.
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les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                               STREET: 405 Lexington Avenue, 64th Floor CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TGAATCCGACCAACC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                COUNTRY: USA
ZIP: 10174-6401
                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                               New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          circular
                                                                                                                                                                                                                                No. 56460250 No. 5646025disk of No. 5646025th America, Inc
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                 05-MAY-1995
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                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08986485 Patent No. 6046030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: WU, SHUJIAN
APPLICANT: SWEET, RAYMOND
APPLICANT: TRUNEH, ALEMSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                               1537 GATCGCAATCCGACCAAC 1554
          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2794 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
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                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                               PPLICANT: TRUNEH, ALEMSEGED
ITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
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                                                              COMPUTER:
                                                                                                               COUNTRY: U:
ZIP: 19482
                                                                                                                                                STATE:
                                                                                                                                                              CITY: VALLEY FORGE
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APPLICATION NUMBER:
                                                                                                                                                                                 STREET:
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                                                                                                                                USA
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956..1108
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618..696
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283..413
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2671..2764
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1789..1842
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                                                           IBM Compatible
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US/08/986,485
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Pred. No. 61;
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Indels

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Matches

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; LOCATION: (1)...(887)
; OTHER INFORMATION: n = A,T,C or
US-09-385-982-497
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1998-03-31
EARLIER FILING DATE: 1998-08-31
NUMBER: 0F SEQ ID NOS: 544
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US-09-385-982-497
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                               US-09-098-219B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-250XX
Sequence 1, Application Patent No. 6441277
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 497
LENGTH: 587
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Patent No. 6262334
                                                                                                                                                                                    Query Match
Best Local (
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                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0701
TELEFAX: 610-407-0701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478 GATCTGAATCTGAACAAC 495
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TELEFAX: v-
846169
                                                                                                  505 GATCCGACTCGGACCAACC 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                  Local Similarity 84.7
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                                                                                                                                1 GATCTGAATCCGACCAACC 19
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                   Application US/09098219B
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88.9%;
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                                                                                                                                                                  Score 14.2; DB
Pred. No. 1e+02;
0; Mismatches
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Pred. No. 66
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US-08-976-259-22
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                                                                                                                     Patent No. 6310000
NUMBER OF SEQUENCES: 142
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                    Sequence 22,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 17-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/098,219B
APPLICATION NUMBER: US/09/098,219B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Barry, Gerard
APPLICANT: Cheikh, No. 6441277dine
APPLICANT: Kishore, Ganesh
TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate
TITLE OF INVENTION: Aldolase in Transgenic Plants
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: MOBT:086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
             ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                           APPLICANT: Choi, Gil H.
APPLICANT: Welch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: F.
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ZIP: 77210-4433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GATCTGAATCCGACCAACC 19
                                                                                                                                                                                                                                                                                                                                                                        22, Application US/08976259
                                                                                                                                                                                                                                                                                                                                                            6316609
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                                                                                                             USA
                                                                                                                                                                                                                                                                                                                  Dillon, Patrick J.
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ASCII Text
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                                                     3.50 inch, 1.4Mb storage
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Pred. No. 1.1e+02;
O: Mismatches 3;
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620A
FILING DATE: 03-CAN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5526-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERÈNCE/DOCKET NUMBER: 1488.0740002/EKS/CBM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2560
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 2916 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
SCOCKACTERISTS: COUBLE
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APPLICATION NUMBER: US
FILING DATE: Herewith
                           SEQUENCE CHARACTERISTICS:
LENGTH: 3671 base pairs
TYPE: nucleic acid
STRANDEDESS: single
model cor. ...
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: A Family of Map2 Protein Kinases NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Boulton, Teri G. APPLICANT: Cobb, Melanie H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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 OLECULE TYPE:
                                                                                                                                          TELEFAX:
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ZIP: 10036
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REGISTRATION NUMBER: 36,688
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Panayotatos, Nikos
                                                                                                                                                : (212) 790-9090
(212) 869-8864/9741
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protein
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Pred. No. 1
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US-08-176-620A-5
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US-08-463-862-5
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Patent No. 577675
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Matches 16; Conserv
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3671 base pairs
                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 16-MAY-1991
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1 GATCTGAATCCGACCAACC 19
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843 GATCTCAAGCCGGCCAACC 861
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                                                        Local Similarity tes 16; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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ZIP: 10036-2711
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                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                      LOCATION:
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/ENTION: A FAMILY OF MAP2 PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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303..2018
                                                           Conservative
                                                                                                                                    303..2018
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                                                                                                                                                                               DNA (genomic)
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84.2%;
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84.2%;
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                                                                          Score 14.2;
Pred. No. 1
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                                                           Mismatches
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                                                                          .3e+02;
                                                                                         DB 1;
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                                                             Indels
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RESULT 13 US-08-461-985-5 ; Sequence 5, Application US/08461985

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US-08-458-887-5
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Best Local :
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                                                                                                                                                                               GENERAL INFORMATION:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
08/176,620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3671 base pairs
TYPE: nucleic acid
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08
FILING DATE: 03-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                 APPLICANT: Boulton, Teri G. et al.
TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
                                                                                                                                                                                                                                                                                                      843 GATCTCAAGCCGGCCAACC 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 65
REFERENCE/DOCKET NUMBER: 100.
                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT: Panayotatos, Nikos
ITLE OF INVENTION: A Family of Map2 Protein Kinases
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TOPOLOGY: unl
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Les 16; Conserv
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                               COUNTRY:
                                                     STATE:
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                     10036-271
                                                               New York
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Y: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yancopoulos, George D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boulton, Teri G. Cobb, Melanie H.
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
303..2018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
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(212) 869-8864/9741
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                                                                                                      Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                    Score 14.2; DB 2;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 3671;
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RESULT 15
US-08-390-888A-2/c
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                       COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/390,888A
APPLICATION NUMBER: US/08/390,888A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
               CLASSIFICATION: 424
ANTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 141
                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: 127 Peachtree Street, N.E., Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MOTZUNOV, Sergey
APPLICANT: KSiazek, Thomas G.
APPLICANT: Rollin, Pierre E.
APPLICANT: Spiropoulou, Christina F.
TITLE OF INVENTION: THE BAYOU HANTAV
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       843 GATCTCAAGCCGGCCAACC 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT:
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ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 02 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                      CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CENGTH:
                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Application US/08390888A 5916754
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                                                                                                                                                                                                                                                                   Georgia
Y: USA
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66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3671 base pairs
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303..2018
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E: DNA (genomic)
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84.2%;
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Pred. No. 1
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TELEPHONE: (404) 688-0770
TELEPAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3677 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: DNA (genomic)
US-08-390-888A-2
T1.0%; Score 14.2; DB 2; Length 3677;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps
OY
1 GATCTGAATCCGACCAACC 19
Db 2053 GAGCTGTATCAGACCAACC 2035
Search completed: May 12, 2003, 02:38:31
Job time: 11.7857 secs
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                            Result
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                               seq length: 0
seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                           Match
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20
                                                gatctgaatccgaccaaccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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:/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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      10 US-09-864-761-1359
10 US-09-815-242-9151
9 US-09-918-995-2350
9 US-09-985-298-4
12 US-10-095-718-3
12 US-10-095-718-3
12 US-09-95-718-3
12 US-09-95-718-3
12 US-09-764-891-9967
9 US-09-764-891-9966
9 US-09-986-791-3071
9 US-09-986-791-3071
9 US-09-9864-761-32024
9 US-09-9864-761-15510
10 US-09-98-842A-1568
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Sequence 2350, Apsequence 43, Appli sequence 3, Appli sequence 1, Appli sequence 9965, Apsequence 9965, Apsequence 1, Appli sequence 3071, Apsequence 794, App sequence 15510, Apsequence 15510, Apsequence 15510, Apsequence 455, Appsequence 6740, Apsequence 6740, Apsequence 6740, Apsequence 8698, Apsequence 8698, Apsequence 8698, Apsequence 8698, Apsequence 8698, Apsequence 3916, Appearaments
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Sequence 9151, Ap
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45	44	43	42	41	40	39	38	37	36	35	34	3	32	31	30	29	28	27	26	25	24	23	22	21	20
13.8	13.8	13.8	14	14.2		14.2								14.2										14.2	14.2
69.0	69.0				71.0	71.0	71.0		71.0	71.0		71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0		71.0	71.0	71.0
271	231	197	657	684973	147309	21129	21129	10900	10846	5510	2916	2632	2604	2318	2179	1407	1372	1275	1080	1006	854	615	572	485	466
10	10	10	10	10	10	10	Ø	10	10	12	10	12	9	9	10	10	9	10	10	10	10	10	10	10	10
US-09-923-876-4684	US-09-960-352-14201	US-09-983-965-4349	US-09-891-171-4	US-09-263-959-1	US-09-742-312-3	US-09-764-869-1734	US-10-091-504-1734	US-09-923-109-6	σs-09-923-109-5	US-10-044-090-353	US-09-956-004-22	US-10-044-090-312	US-09-938-842A-458	US-10-260-046-29	US-09-867-550-1891	US-09-898-932-1	US-09-938-842A-2894	us-09-974-300-917	US-09-923-109-1	US-09-770-445-227	US-09-925-300-382	US-09-974-300-4348	US-09-974-300-1878	US-09-917-800A-585	US-09-864-761-14634
Sequence 4684, Ap	Sequence 14201, A	43	Sequence 4, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 1734, Ap	Sequence 1734, Ap	Sequence 6, Appli	Sequence 5, Appli	Sequence 353, App	Sequence 22, Appl	Sequence 312, App	Sequence 458, App	Sequence 29, Appl	Sequence 1891, Ap	Sequence 1, Appli	Sequence 2894, Ap	Sequence 917, App	Sequence 1, Appli	Sequence 227, App	٠.	Sequence 4348, Ap	Sequence 1878, Ap		Sequence 14634, A

ALIGNMENTS

; Sequence 13599, Application US/09864761
; Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.

US-09-864-761-13599

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APPLICANT: Genc. Menshang Genome-Derived Single exon nucleic acid probes useful title of invention: Gene expression analysis by microarray file reference: Acomica-y.1

CURRENT APPLICATION UNDER: US/09/864.761

CURRENT PILLING DATE: 2001-05-23

PRIOR APPLICATION UNDERS: US 60/180,312

PRIOR APPLICATION UNDERS: US 60/207,456

PRIOR APPLICATION UNDERS: US 60/207,456

PRIOR ETILING DATE: 2000-02-04

PRIOR APPLICATION UNDERS: US 09/632,366

PRIOR APPLICATION UNDERS: US 09/632,366

PRIOR PRILING DATE: 2000-09-03

PRIOR APPLICATION UNDERS: US 09/632,366

PRIOR FILING DATE: 2000-09-03

PRIOR APPLICATION UNDERS: US 60/236,359

PRIOR APPLICATION UNDERS: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION UNDERS: PCT/US01/00667

PRIOR APPLICATION UNDERS: PCT/US01/00667

PRIOR APPLICATION UNDERS: PCT/US01/00669

PRIOR APPLICATION UNDERS: PCT/US01/00668

PRIOR APPLICATION UNDERS: PCT/US01/00669

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; OTHER INFORMATION: MAP TO ACC23314.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
US-09-864-761-13599
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2001-01-29
                                                               ; LOCATION: (1)...(1005)
US-09-815-242-9151
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13599
LENGTH: 5359
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                SEQ ID NO 9151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9151, Application US/09815242 Patent No. US20020061569A1
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS; 14110
SOFTWARE: FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                 ORGANISM: Streptococcus pneumoniae
                                                                                                   NAME/KEY: CDS
                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zyskind, Judith W.
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  79.0%;
89.5%;
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; Pred. No. 1.1e
0; Mismatches
  Score 15.8; DB 10;
Pred. No. 1.1e+02;
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                      Length 1005;
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Hyseq Inc.

PITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

ITILE OF INVENTION: FROM VARIOUS CNA LIBRARIES

FILE REPERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2350

LENGTH: 457

TYPE: DNA

ROANISK: Homo sapiens
                                                                                                                       ; SEQ ID NO 43;
LENGTH: 2460;
TYPE: DNA;
ORGANISM: Homo sapiens
US-09-895-298-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE: misc_feature
, NAME/KEY: misc_feature
; LOCATION: (1)...(457)
, OTHER INFORMATION: n = A,T,C
US-09-918-995-2350
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                  δÃ.
                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/895,298
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 09/591,16
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: PCT/US99/29950
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/113,006
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 231
NUMBER OF SEQ ID NOS: 231
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US-09-895-298-43
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Best Local Similarity
Matches 17; Conserv
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Best Local :
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TITLE OF INVENTION: 47 Human Secreted Proteins
FILE REFERENCE: PZ035P1
                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 GAACTGAATCAGACCAACTG 161
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1 GATCTGAATCCGACCAACCG 20
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85.0%;
                                                        76.0%; Score 15.2; I
85.0%; Pred. No. 2.20
tive 0; Mismatches
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Pred. No. 2.
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                                                                                         Length 2460;
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2175 GAACTGAATCAGACCAACTG 2194

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US-10-095-718-3/c
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LENGTH: 7914
TYPE: DNA
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                                                             SEQ ID NO 1
LENGTH: 7944
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APPLICANT: Munson, Keith
TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 35052/204375
CURRENT APPLICATION NUMBER: US/10/095,718
CURRENT FILING DATE: 2002-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Walsh, Christopher
APPLICANT: Chao, Hengjun
APPLICANT: Burstein, Haim
                                                                                                                             CURRENT APPLICATION NUMBER: US/10/095,718
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION UNMBER: 09/689,430
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/158,780
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 5
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NUMBER OF SEQ ID NOS: 5
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                                                                                                                                                                                                                                                                                       APPLICANT: Stepan, Tony
APPLICANT: Munson, Keith
TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 35052/204375
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chao, Hengjun
APPLICANT: Burstein, Haim
                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/689,430
PRIOR FILING DATE: 2001-08-22
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LOCATION: (435)...(4730)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                  ORGANISM: Artificial Sequence
                                          TYPE: DNA
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Local Similarity 85.0%;
hes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Christopher
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Pred. No. 2
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US-09-764-891-9966
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Query Match
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                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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US-09-764-891-9967
; Sequence 9967, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and
; FILE REFERENCE: PC006
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
                                   NAME/KEY: SITE
LOCATION: (4480)
OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (4483)
OTHER INFORMATION: n e
US-09-764-891-9966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (420)...(4835)
US-10-095-718-1
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Best Local Similarity
Matches 17; Conserv
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LENGTH: 19929
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver.
SEQ ID NO 9966
LENGTH: 20907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4920 GATCTGGATCCGAACAAACG 4901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                  OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                      NAME/KEY: SITE LOCATION: (4477)
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85.0%;
                                                       equals a,t,g, or
                                                                                                                     equals a,t,g,
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76.0%;
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Pred. No. 2.2e+02;
Score 15.2;
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Length 20907;
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; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-939-964-1
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US-09-918-995-794
                                                                        B
                                                                                                                                                                                                                    ; TYPE: DNA; Homo sapien US-09-867-701-3071
               RESULT 11
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Matches 17
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APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 536165
                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3071
EINCTH: XX37
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Best Local Similarity
Matches 17; Conserv
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Matches
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Publication No. US20030054522A1
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/214,808
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Periet, Xavier Philippe
APPLICANT: Broughton, William John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic TITLE OF INVENTION: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18962 GAACTGAATCAGACCAACTG 18981
                                                                        309 GATCTGAATCTGAACAAC 326
                                                                                                                                                Local Similarity
nes 16; Conser
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17; Conserva
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85.0%;
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Pred. No. 2.3e+02;
0; Mismatches 3;
                                                                                                                                              Score 14.8; DB 10;
Pred. No. 3.4e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.3e+02;
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION WEBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
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US-09-864-761-32024/c
US-09-864-761-32024/ Application US/09864761
Sequence 32024, Application US/09864761
Patent No. US20020048763A1
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NAME/KEY: misc_feature

; LOCATION: (1)...(479)

; OTHER INFORMATION: n = A,T,C

US-09-918-995-794
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Best Local (
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION UNMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
                                                       PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
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Hanzel, David K.
Chen, Wensheng
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Pred. No. 3
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RESULT 14
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
PRIOR REPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR REPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR REPLICATION NUMBER: US 09/774,203
PRIOR REPLICATION NUMBER: US 09/774,203
PRIOR REPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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Best Local S
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SEQ ID NO 1568
LENGTH: 732
TYPE: DNA
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LENGTH: 560
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APPLICANT:
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Xun
APPLICANY: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
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APPLICANT: Kreps, Joel
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OTHER INFORMATION: EXPRESSED IN BT474,
OTHER INFORMATION: EXPRESSED IN LUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
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                                                         504 ATCTGATTCCGACCCACC 487
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INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.99
INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.99
INFORMATION: EXPRESSED IN LACENTA, SIGNAL = 1.2
INFORMATION: MITH: ALIGNOTA, EVALUE 0.00e+00
INFORMATION: EST_HUMAN HIT: BE082541.1, EVALUE 0.00e+00
INFORMATION: SWISSPROT HIT: P48552, EVALUE 1.00e+106
                                                                                                                                               16; Conserv
                                                                                                                                               Conservative
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NUMBER: PCT/US01/00670
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88.9%;
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88.9%;
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Pred. No. 3
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Pred. No. 3
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1.4e+02;
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                                                                                    Matches
                                                                                                                              Query Match
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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PRIOR APPLICATION NUMBER: PCT/US01/00661
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PRIOR APPLICATION NUMBER: PCI/US01/00667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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OTHER INFORMATION: EXPRESSED IN B7474, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
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600 ATCAGAATCTGACCAACC 583
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                                                                                    Similarity 88.1
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RESURD 15
US-09-770-444-455
Sequence 455, Application US/09770444
Patent No. US200003280Al
RESURAL INFORMATION: John APPLICANT: Gorlach, Carol M.
APPLICANT: Gorlach, Carol M.
APPLICANT: Hamilton, Carol M.
APPLICANT: Hamilton, Carol M.
APPLICANT: Rameaka, Joshua G.
APPLICANT: Rameaka, Joshua G.
APPLICANT: Rameaka, Joshua G.
APPLICANT: Hamilton, Carlos A.
APPLICANT: Hamilton, Carlos A.
APPLICANT: Hamilton, Patrick
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APPLICANT: Hamilton, Patrick
APPLICANT: Hamilton, Patrick
APPLICANT: Salder, Ted
APPLICANT: States, Majia
APPLICANT: States, Majia
APPLICANT: Hamilton, Patrick
APPLICANT: Hamilton,
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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Result No.	Score	Query Match Length DB	Length	DB	מו	Description
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ALIGNMENTS

CUS	BH210086 687 bp DNA linear GSS 24-OCT-2001
1	sequence.
CESSION	BH210086
RSION	BH210086.1 GI:16389299
YWORDS	GSS.
URCE	Schistosoma mansoni.
ORGANISM	Schistosoma mansoni
	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
	Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
FERENCE	1 (bases 1 to 687)
AUTHORS	Shetty, J., Simpson, A., Malek, J., Koo, H., LoVerde, P.T. and El-Sayed
	, N.M.
TITLE	Use of end sequences from Schistosoma mansoni (Puerto Rico strain)
	Sml BAC library for gene discovery and map construction
JOURNAL	Unpublished (2001)
MMENT	Other_GSSs: Sm1-56J20.TR
	Contact: Najib M. El-Sayed
	Department of Eukaryotic Genomics
	The Institute for Genomic Research
	9712 Medical Center Dr., Rockville, MD 20850, USA
	Tel: 301 838 0200
	Fax: 301 838 0208
	Email: nelsayed@tigr.org
	Lo.edu).
	Class: BAC ends.

GSS 13-DEC-2000

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REFERENCE
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TITLE
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Unpublished (2001)
Other GSSs: BOGNU32TF
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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Brassica oleracea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BH526706
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                   Conservative
                                                                                                                                                                                                                                                                                               sheared ends.
                                                                                                                                                                                                                                                                                                                                                  cdtown@tigr.org
                                                                                                         /clone_lib="BOGN"
/note="Vector: pHOS1; Site_1: Bs
genomic DNA inserted into pHOS1
genomic DNA inserted 283 t
                                                                                                                                                                                                  /organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
                                                                                                                                                                                                                                                             1. .838
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/clone="Sm1-56J20"
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/strain="Puerto Rico"
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                               Score 16.8; DB 17; Pred. No. 3.5e+02;
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                                                                                                                                                                                                      sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CE10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAIIG10P 528 bp DNA T. brucei sheared genomic DNA clone 11g10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trypanosoma brucei
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                   1 (bases 1 to 640)
El-Sayed, N., Zhao, S., Zha
Gerrard, C., Leech, V., de
, Fraser, C. and Adams, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma bruces
Determination of clone end sequences from Trypanosoma brucei TREU
                                                                                                                          Trypanosoma
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927P1-8A1.TV
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                                                                                                         Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                Trypanosoma
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                                                                                                                                                                                    AQ638867.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="11g10"
155 c 118 g 133 t
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                                                                                                                                                  brucei.
                                                                                                                                                                                    GI:5115577
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                                                                                                                                                                                                                                     640 bp DNA linear GSS 08-JUL-1999 927Fl Trypanosoma brucei genomic clone 927Fl-8A1, DNA
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                                   Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
de Jong,P., Ullu,E., Melville,S., Donelson,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 17;
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Unpublished (1999)
Other_GSSs: 927Pl-8A1.TP
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGAACCCGACCAACCG 396
                                                    Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                 Unpublished (2001)
On Dec 18, 2000 this sequence version replaced Contact: Wing RA
                                                                                                                                                                                                             Triticeae; Hordeum.

1 (bases 1 to 696)

Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu, Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W., Fenton,R.D. and Main,D.

Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                            Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae
                  Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF621944 696 bp mRNA linear EST 1' HVSMEa00001F16f Hordeum vulgare seedling shoot EST library HVcDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSME
                                                                                                                                                                                               for barley genomics: Morex cold-stressed seedling shoot cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: neleayedetigr.org
For clone/filter availability, please contact Sara Melville
(smi60@mole.bio.cam.ac.uk). Pl end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
                                                                                                                                                                                                                                                                                                                                                                                                      Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pAD10SacBII; Site_1: Bam H1; Constructed by Sara Melville, University of Cambridge, UK and Nancy Shepherd, Dupont Merck, Wilmington, DE. Genomic DNA was isolated from Trypanosoma brucei (stock TREU927/4) and partially digested with Sau 3AI. DNA fragments were cloned into the Bam H1 site of pAD10SacBII vector (Genbank accession U09128). The average insert size is 65 Kb. Coverage: approx 4.4 X the haploid non-minichromosomal genome."
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/strain="TREU927/4"
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BH516307
                                                                                                        Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other GSSS: BOGKX42TR
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BOGKX42TF BOGK Brassica oleracea
                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                       Brassica oleracea
                                                                                  Contact:
                                                                                                                                                                                                    1 (bases 1 to 647)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                               Brassica oleracea.
                                                                                                                                                                                                                                                                                                                                                                                                                                            BH516307.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
Medical Center Drive, Rockville, MD 20850, USA 301-838-3523
                                                                                  Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 were in vivo excised to give pBluescript SK(-) CDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             this clone see http://www.genome.clemson.edu/orders Also
see close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anobored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxine in covered crystallization dishes. Five-day old seedlings were incubated at SoC for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 600000 pfu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
146 c 197 g 170 t
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/db_xref="taxon:4513"
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94.4%;
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Pred. No. 5.2e+02;
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Other_GSSs: RPCI-24-377116.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0208
Fax: 301 838 0208
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1 (bases 1 to 745)
Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://ww.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
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/note="Yector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
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730 CTGAATCCGACCAACC 745
33 ATCTGAATCCGACCAA 48
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16; Conserv
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Entamoeba histolytica
Eukaryota, Entamoebidae, Entamoeba.
1 (bases 1 to 909)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 48
High quality sequence stop: 770
Location/Qualifiers
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BH130484
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ENTOL69TF Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HM1: IMSS sheared DNA library (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Loftus, B., Wang, Z., Van Aken, S. and Fraser, C. Determination of clone end sequences from Ent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH130484.1 GI:15088953
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Clones are derived from t
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                                                                               Conservative
                                                                                                                                                                            /clone_lib="Entamocha histolytica Sheared DNA"
/clone_lib="Entamocha histolytica Sheared DNA"
/note="Vector: pHOSI; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamocha histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Pred. No.
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ches 0;
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AUTHORS
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                                                                                                                                                                                         69 ATCTGAATCCGCCCAACAG 51
                                                                                                                                                                                                                                   2 ATCTGAATCCGACCAACCG 20
234 bp mF
BB398677 RIKEN full-length enriched,
clone C330009I19 3', mRNA sequence.
BB398677
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Un, S., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Parson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritte. Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G(I)/G(S)/G(T) BETA SUBUNIT 1 ;, mRNA sequence.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
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                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI; Original library was constructed in lambdaZIPLOX: Nexcision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."

43 c 51 g 42 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="zebrafish adult brain"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="5332800"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Danio rerio"
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89.5%;
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d, ES
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                                                                                                                                                                                                                                                                                                                                Length 184;
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1 (bases 1 to 234)

8 Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Itoh, M., P., Endo, T., Fukuda, S., Fukunishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Yano, R., Tasunishi, A., Tokota, T., Yanamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Haysshizaki, Y.
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EST.
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URLihttp://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
Trehalose and its application for the synthesis of full length
trehalose and its application for the synthesis of full length
cDNA, Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
v and Hayashizaki v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carrinot, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Unpublished (2000)
Contact: Yoshihide Hayashizaki
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/note="Site_1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RIKEN full-length enriched, ES cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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Query Match
Best Local Similarity

79.0%; 89.5%;

Score 15.8; DB 10; Pred. No. 7.4e+02;

Length 234

B, δā.

BB357524

LOCUS

SOURCE KEYWORDS

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REFERENCE
AUTHORS
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Hirozane, T., Hori, F., Ishi, Y., Ishikawa, T., Ishikawa, T., Ishikawa, T., Ishikawa, T., Kiwuchi, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, M.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
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Suzuki, H., Suzuki, H., Taqawa, A., Takahashi, F., Tominaga, N., Toya
T., Tsunoda, Y., Watahki, A., Watanabe, S., Yamamura, T., Yananaka, I.
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Konno, H., et al.)
L. Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci_P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB357524 256 bp mRNA linear EST 12-JUL-2000 BB357524 RIKEN full-length enriched, adult male corpus striatum Mus musculus cDNA clone C030021K24 3' similar to X14897 Mouse fosB mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                ,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninoi,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                    further details
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/tissue_type="corpus striatum"
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/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                                                            striatum
                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                   'sex="male"
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Fax: (204) 983-4604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloutier, S.
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COMMENT

FEATURES

Score 15,8;

DB 14; Length 285;

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Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Coreal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
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/noti="Vector: pSPORT-P (Invitrogen Technologies);
/note="Vector: 
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Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Triticum aestivum"
/cultivar="Glenlea"
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/clone="mage05031g01f"
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   EBro02_SQ002_I18_R root,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: walbotestanford.edu
Possible ligation site of ends cut
Reverse complemented post-ligation
Plate: 1006119 row: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 650 723 2227
Fax: 650 725 8221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Walbot V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize genomic sequences found using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transposon-tagged
                                                                                                                                                                                                                                                                                       Inote-"Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, 90 to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and 1911, and 19ated to form circular plasmids. DH10B and BglII, and 19ated to form circular plasmids.
                                                                                                                                                                                                                                             ampicillin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
                                                                                                                                                                                                                                                                           cells were transformed and then screened on LB plates with
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Pred. No. 8.
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302 bp mRNA linear
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8.1e+02;
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On Feb 1, 2002 this sequence version replaced gi:18473872.
Contact: Waugh R, Marshall DF
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 328) Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., P., Endo,T., Hori,F., Ishil,Y., Ishikawa,J., Ishikawa,J., Ishikawa,J., Ishikawa,J., Ishikawa,J., Kadota,K., Kagawa,I., Kaj.C., Kawai,J., Kawai,J., Kuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
                                                                                                                                                                                                                                                                                                                                                                          BB297513 328 bp mRNA linear EST 10-UUL-2000 BB297513 RIKEN full-length enriched, 9.5 days embryo parthenogenote Mus musculus cDNA clone B130055M05 3', mRNA sequence.
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Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
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Development of Barley Transcriptome Resources
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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BB297513.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Function) project.
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cv Optic, EBro02"
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/dev_stage="3 week"
/lab_host="DH10B"
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/db_xref="taxon:4513"
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89.5%;
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Search completed: May 12, 2003, 02:35:23 Job time: 249.143 secs
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Itoh.M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki,                                                                                                                                                                                                                                                                                                                                                          l Similarity
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-9216
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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parthenogenote"
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Post-processing: Minimum Match 0%
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Pred. No.

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the number of results predicted by chance to have a

KEYWORDS SOURCE ORGANISM

REFERENCE

S.mansoni (strain Egyptian) DNA, clone pSm1-7.
Schistosoma mansoni
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 121)
Hamburger, J., Turetski, T., Kapeller, I. and Deresiewicz, R.
Highly repeated short DNA sequences in the genome of Schistosoma mansoni recognized by a species-specific probe

RESULT 1
SCMRPTAA/C
LOCUS
DEFINITION
ACCESSION
VERSION

121 bp S.mansoni tandem repeat units. M61098 M61098.1 GT:161064

DNA

linear

INV 26-APR-1993

ALIGNMENTS

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tamerisa,K., Tamerisa,K., Tamerisa,K., Tamerisa,K., Tamerisa,Tamsey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wheczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,JJ., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J.,
Earnhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M.,
Earnhart, B., Edwards, C., Elhaj, C., Escotto, M.,
Earnhart, C., Edgar, D., Edwards, C., Ford, J., Foster, P., Frantz, P.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J. H., Guevara, W., Gunaratue, P., Hale, S., Hamilton, K.,
Gorrell, J. H., Guevara, W., Gunaratue, P., Hale, S., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollis, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollis, B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20;
Pred. No.
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, *** SEQUENCING IN PROGRESS ***,
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Center: Baylor College of Medicine Center code: BCM
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(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* consists of 59 contigs. The true order of the pieces

* took known and their order in this sequence record is
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Direct Submission
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INV 15-MAR-2002

Score 17.4; DB 2; Length 146970; Pred. No. 2e+02;

2e+02;

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Bukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;

Neotaenioglossa; Cerithioidea; Scaliolidae; Scaliola.

1 (bases 1 to 1356)

Lydeard,C., Holznagel, W.E., Glaubrecht, M. and Ponder, W.F.

Lydeard,C., Holznagel, W.E., Glaubrecht, M. and Ponder, W.F.

Molecular phylogeny of a circum-global, diverse gastropod superfamily (Cerithioidea: Mollusca: Caenogastropoda); pushing the deepest phylogenetic limits of mitochondrial LSU rDNA sequences Moll. Phylogenet. Evol. 22 (3), 399-406 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                        100685 bp DNA linear PLN 13-SEP-2000 Arabidopsis thaliana chromosome I BAC F1B16 genomic sequence, complete sequence.
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Lydeard.C., Holznagel,W.E., Glaubrecht,M. and Ponder,W.F.
Direct Submission
Submitted (17-0CT-2000) Biodiversity and Systematics, Department of Biological Sciences, The University of Alabama, Box 870345, Tuscaloosa, AL 35487-0345, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scaliola sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes with similarity to proteins in the databases are named 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described a 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The gene prediction programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory,
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Bases 1-32,040 of IGF clone FIB16 overlap with bases 97,508-129,547 of IGF clone F10A5, gb/AC006434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A.
and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (17-FEB-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-SEP-2000) I
Stanford University, 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-MAR-2000) DNA Sequencing and Technology Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Denmark,http:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://compbio.orni.gov/section/index.html), GENSCAN (http://genes.mit.edu/GENSCAN), FEXA (Victor Solovyev.http://genomic.sanger.ac.uk/ygf/gf.shtml), and NetPlanthtp://genomic.sanger.ac.uk/ygf/gf.shtml) http://genomic.sanger.ac.uk/ygf/gf.shtml) http://genomic.sanger.ac.uk/ygf/gf.shtml) http://genomic.sanger.ac.uk/ygf/gf.shtml) http://genomic.sanger.ac.uk/ygf.gf.shtml) http://gf.gf.shtml) http://gf.gf.shtml) http://gf.gf.shtml http://gf.gf.shtm
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                                                                                     /note="overlap with bases 97,508-129,547 F10A5, gb/AC006434. See GenBank record : F10A5 for annotation in this region."
complement(32986. .33822)
/gene="F1B16.1"
                                                                                                                                                                                                                                                                                     /clone="F1B16"
                                                                                                                                                                                                                                                                                                                                                                               'db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .100685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     et al., CBS, Technical University of p://www.cbs.dtu.dk/NetPlantGene.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               correspondence: arab@sequence.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing and Technology Center, 5 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and NetPlantGene (S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENSCAN (Chris Burge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yu,G., Ecker,J.,
                                                                                                                                             7 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Howng, B., Kim, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hansen, N.F.,
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, CA 94304,
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                                                                                                                                        clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The
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/translation="MEDFRVRHECSSLEGTLLDSKYAKAVQCLVEEVIDIGGRKVELC NIILLNQLFFGRRRGFALSSELKSSLCSSGFWSLFENHEIHIKITKLLSLLQQVEER FEDYCONQLEQVISSFEELAGEGSSKYVTGLALAMFRHFGSLEEALISQLMSVRRRFI ISSHCSTANGEGSSKYVTGLALAMFRHFGSLEEALISQLMSVRRRFI ISSHQDVFKIISSGLSQLSLFDGNTTSSSLQRLGLVQGFQRHAWKFIRGLFETSVAILR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MTSSFLLLTFAICKLIIAVGLNVGPSELLRIGAIDVDGHFTVHP
SDLASVSSDFGMLKSPEEPLAVLHPSSAEDVARLVKTAYGSATAFPVSARGHGHSING
QAAAGRNGVVVEMNHGVTGTPKFLVRPDEMYVDVWGGELWVDVLKKTLEHGLAPKSWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSFRCSSSSFSEKHHNAKSPKSDDIVELPLFPLPLVLFPGAILPLQIFEFRYRIMMH
LLQSDLRFGVVYSDSVSGSAAEVGCVGEVVKHERLVDDRFFLVCKGQEKFRVTNVVRT
KPYLVGEVTWLEDRPSGEENLDSLANEVEVLMKEVIRLSNRLNGKAEKEVQDLRRNQF
                                                                                                                                                                                                                                                                          complement(join(54491. .55074
55872. .56014,56253. .56307))
/gene="F1B16.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="masssgapsrktlsklatnrlokelvemomnpfigfkhkvfidnlok
RWIIEVIGAPGTLYANDTYQLQVDFPEHYPMESPQVIFLHPAPLHPHIYSNGHICLDI
LYDSWSPAMTVSSICISILSMLSSSTEKQRFTDNDRYVKNCKNGRSPKETRWWFHDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(46848.
47773. .47875,47963. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHKAELKLRSKNIWEVPHPWLNLFYPKSRISDFDKGVFKGILGNKTSGPILIYPMNKD
KWDERSSAVTPDEEVFYLVALLRSALTDGEETQKLEYLKDQNRRILEFCEQAKINVKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYLYLTVGGTLSNAGISGQAFHHGPQISNVLELDVVTGQFGIITRARISLEPAPQRVR
WIRVLYSSEKVFTEDQEYLISMHGQLKFDYVEGFVTODEGLITRARISLEPAPQRVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(32986. .33822)
/gene="F1B16.1"
                          NYVKYLPKILWWIHEMRGHYFNADLYKHLPFYAGAMIDSHATAGYWKNRTQARLGIKM
PKTYVYHLGNSKELMEVAEDSVAKRYLREHYRESLGYRNEDLLPGIINSVSRGKGQDL
                                                                                   /translation="MGTDGFVVSICINSVYDSRGPLLLMELAFLLRGVGADVVWITNQ
KPLEDDEVVYSLEHKMLDRGVQVISAKGQKAVDTSLKADLIVLMTAVAGKWLDAVLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52291.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSVSSNGSVLYCLEITKNYHDSDSEIVDQEVEILMKKLNFIPTSVFTTDLQYVDFLDR
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46200. .465
                                                                                                                                                                                                                                                                                                                                                                                                        complement (54491. .56307)
                                                                                                                                                                                                                                                                                                                                                                                                                                          FRRTKYTPLNLILLFF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AWLFQHFLHPSVFLLLKCNNTSDESKLKCWRNNISLIAVMKTVIRMKQRSWCWRLKQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(52291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YLPHHATQEEWVAHFGDKWDRFRSLKAEFDPRHILATGQRIFQNPSLSLFPPSSSSSS
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/db_xref="GI:10120443"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTPFSFFYGSTFEGAPREQQALLELEDTAARLKRERETLRNTLNYLTAASAYKDYFPS
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/translation="MALPHYVSSPSSTSLSPSEKSKPPEHSLRSLSPTYDNRRRCKLN
FLRAFHESLERTKEKKLQVPTMHAVVVGSDMSKQTKFETELRNFVREKKLENFVHFVN
                                                                                                                                                                                                                                               'note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                              /gene="F1B16.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAG13063.1"
/db_xref="GI:10120438"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F1B16.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="FIB16.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product="Putative ubiquitin-conjugating enzyme"
'protein_id="%AAG13066.1"
'db_xref="GI:10120441"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F1B16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F1B16.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mote="Similar to cytokinin oxidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F1B16.2"
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                                                                                                                                                  /protein_id="AAG13070.1"
/db_xref="GI:10120445"
                                                                                                                                                                                                                     cocon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Hypothetical protein"
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.48066,48156. .
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.48185))
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KTLTVAPYIAAIDVLVQNSQARGECFGRITIEAMAFKLPVLGTAAGGTMEIVVNGTTG

Mb of DNA sequence

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RESULT 5
HUACO02990
LOCUS
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AUTHORS
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Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R., Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L. Deslattes Mays,A., C20,Y., Xu,R.X., Kang,H.L., Mitchell,S., Bichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.
                                                                                                                                                                                                                                                                        ниасии2990 106760 bp DNA linear PRI 23-NOV-1999
Human Chromosome 16 BAC clone CIT987SK-A-1000D7, complete sequence
AC002990
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 106760)
                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                   Homo sapiens.
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//do.kref="GI:10120440"
//do.kref="GI:10120440"
//do.kref="GI:10120440"
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GDVRNUENVFIPPTSDVAVNGNVTVSSNDLSFHGGGLSLSLGNQTIQSAVSVSPFQYHY
QNLSNQLSYNNLNFSTMSDENGKSLSVHQHBSDQILPSSVYNNNCHGQPFHNGSSDMTTEDD
TSGFVSSVLARFXLKPTQCLLDEVVSYRXDLKLGNKKKKNLGQPFHNGSSDMTTEDD
TSGSVSSVLARFXLKPTQCLLDEVVSYRXDLKGNSKKKKLLTMVDEVDKRYNQYHQMEALASSFEMYTGLGAAKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(69063. .69566)
/gene="F1B16.8"
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/db_xref="GI:10120442"
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/db_xref="GI:10120442"
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/translation="MppRaIRVSOEDLSQKSATPEMSTNSMYPDSSGSSLASSDLIEV
RMSIGSERGTLSEGGTPPDGHLGTPASQKSATPEMSTNSMYPDSSGSSLASSDLIEV
RMIYDDSPGIVPSAQSKPLESTBSLSWFSULSTCSNUTPATGSQYASSEGGWSKMYTTSEELV
RYSQRDRWSFDSEHLGSGRRKLSGGSSRFSFSPSVVDQQVCGACSKLLTERSSIATFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(62425. .63429,63528. .63559,63863. 64640. .64698))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAG13064.1"
/db_xref="GI:10120439"
/translation="MGSSTSGNCSSVSTTGLANSGSESDLRQRDLIDERKRKRRQSNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(69063. .69566)
/gene="F1B16.8"
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KQYKRCKNRVVDSYGESECDEFVFQKMGKREGKALKLEASCSSKSSSNKSFLKWHFAS
ISSKWNKPSSKDSALKKGFWSRHRNNRSSSSIEVKIHTLNIQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F1B16.7"
/note="hypothetical protein"
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ALHQQLGMYRPAWRDQRGLPENSYSILRAWLFEHFHFPYRKESEKINLKKRDYGLSKNQ
VANWFINARVELWKRWIEEMYKEEFGERAELLKSNSODYKKNGETSQLKHEDSSSSOQ
QNQGNNNNNIFYTSDAEQNLVFADPKFDRATTGDYDSLMNYHGFGIDDYNRYVGLGNQ
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/codon_start=1
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/gene="F1B16.6"
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/gene="F1B16.6"
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                                                                                                                          ATATTAACGCCCACGCTCTC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hgi/hgi.html). Genes without pepetide homolgy and spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medical Center Dr., Rockville, MD 20850, USA
on Jan 28, 1998 this sequence version replaced gi:2809277.
Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA e-mail address: mdadams@tigr.org. The orientation of the sequence is from methods including: XGRAII (available by a combination of five methods including: XGRAII (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://grommio.stanford.Edu/\chis/GENSCANW.html)searches of the http://grommio.stanford.Edu/\chis/GENSCANW.html)searches
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Submitted (03-OCT-1997) The Institute for Genomic Research,
Medical Center Dr., Rockville, MD 20850, USA
4 (bases 1 to 106760)
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Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J.,
Brandon, R., Kim, U.J., Kerlavage, A.R. and Venter, J.C.
Human Chromosome 16 BAC clone CIT987SK-A-1000D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from human chromosome 16p and
Genomics 60 (3), 295-308 (1999)
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/db_xref="taxon:9606"
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105684. .105815
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Rattus norvegicus clone CH230-91018,
***, 56 unordered pieces.
                                                                                        Submitted (02-AUG-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Aug 1, 2002 this sequence version replaced gi:22001463.
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Contact: hgsc-help@bcm.tmc.edu
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8, *** SEQUENCING IN PROGRESS
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                          Direct Submission
Direct Submission
Submitted (26-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Raylor Plaza, Houston, TX 77030, USA
Submitted (15-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Apr 27, 2002 this sequence version replaced gi:19718590.
                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (13-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 168949)
                                                                                           of Molecular and Human
Baylor Plaza, Houston,
5 (bases 1 to 168949)
                                                                                                                          Submitted (27-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
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Baylor USA

Delaney, K. R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Hernandez, J., Hernandez, O., Hodyson, A., Hogues, M., Holloway, C.,
Hellins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Lewis, L., Li, J., Li, Z., Martin, R., Martinadle, A.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,
Meison, D., Newtson, J., Newtson, N., Nguyen, N., Nguyen, N.,
Nickerson, E., Nwarton, J., Newtson, N., Nguyen, N., Nguyen, N.,
Nickerson, E., Nayaton, B., Peery, J., Peters, L., Peters, L., Oviedo, R., Pace, A., Payton, B., Peerey, J., Perez, L., Peters, L., Oviedo, R., Pace, M., Parton, B., Peerey, J., Perez, L., Rives, M., Ren, Y., Rives, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Skooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Skitton, A., Svatek, A., Stanley, H., Stone, H., Skitton, A., Svatek, A., Stanley, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Wu, Y., Walliamson, A., Wheczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstock, G. and Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N. E. Buhay, C., Burch, P., Burkett, C., Burrell, K. L., Byrd, N. C., Carron, T. F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C. D., Cox, C., Coyle, M. D., Dathorne, S. R., David, R., David, M. L., Davis, C., Davy-Carroll, L., Dederich, D. A., Davis, C., Davy-Carroll, D. A., Davy-Carroll, D. A., Davis, C., Davy-Carroll, D. A., Davis, C., Davy-Carroll, D. A., Davy-Carroll, D. A., Davy-Carroll, D. A., Davy-Carroll, D., Davy-Carroll, D. A., Davy-Ca Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 16949)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bryant, N.P.,

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SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
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STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
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gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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complement(388. .505)
/rpt_family="L2"
1269. .1360
                            complement(10685..11011)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 184321)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 3, clone RP11-553K23
                                                                                                                                                                                                          ACU25890 184321 bp
Homo sapiens chromosome 3 clone
SEQUENCE, 4 unordered pieces.
ACU25880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                      AC025890.3 GI:8077134
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 90.
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(13485.
/rpt_family="MIR"
13574. .13648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="THEIC"
complement(29224. .29691)
/rpt_family="THEIC"
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/rpt_family="L2"
complement(12392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_fami
26537. .2
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15731. .15760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="MIR" complement(14657. /rpt_family="MIR"
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21914. .22316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="MLTID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="L1PA10"
complement(2007)
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complement(28315...28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="MIR" 27763. .27794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="124589. .24730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="MER5B"
17452. .17662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_family-"MLT1D"
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5, .2071"
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90.0%;
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7445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ly="AT_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.8; DB 9;
Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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3 map 3,
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WORKING DRAFT
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FEATURES

QUALSTAT-REPORT.

ocation/Qualifiers

source

misc_feature

.1999

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repeat_region repeat_region repeat_region repeat_region

/rpt_family="MIR" 3303. 3347

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complement(7615. .7924)
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complement(3360. .3455)
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/rpt_family="CT-rich"

/rpt_family="AluJb" 8780. .9226

/rpt_family="L2"

repeat_region repeat_region repeat_region

rpt_family="(TC)n"

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliew, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Larcoque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Raymond, C., Riley, R., Rogvy, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogvy, P., Rothman, D., Stange-Thomann, N., Schauer, S., Severy, P., Spencer, B., Sentos, R., Schauer, S., Taveres, M., Tridpilo, J., Yessiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vong, G., Zainoun, J., Zimmer, A. and Zody, M.
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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRoque, K., Lamazares, R., Landers, T., Leboczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrin, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C., H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Kiley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, V.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 184321)
Birren, B., Linton, L., Nusbaum, C., Lander, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced gi:7387411. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson, S., Baldwin, J.,
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                                                                                                        Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 181869 bases at least Q40 Consensus quality: 183483 bases at least Q30 Consensus quality: 183879 bases at least Q30 Consensus quality: 183879 bases at least Q30 Consensus quality: 183879 bases at least Q30
Insert size: 215000; agarose-fp
Insert size: 184021; sum-of-contigs
Quality coverage: 4.8 in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                             Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                          Center clone name: 553_K_23
                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: L8244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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AK027375/c
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            REFERENCE
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                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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COMMENT

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Query Match
Best Local Similarity
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3226 bp mRNA linear PRI 01-AUG-2002

HOMO Sapiens cDNA FLJ14469 fis, clone MAMMA1000897, weakly similar

to INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR.

AK027375
                                              Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Shit,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T. Nabohari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T. NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                     AK027375.1 GI:14042008
oligo capping; fis (full insert
Homo sapiens mammary gland cDNA
                                                                                                                                                                                                                                   Isogai,T., Qta,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                               clone:MAMMA1000897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This record will be updated with the finished sequence
(bases 1 to 3226)
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97752 1843:
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18708 53507: contig of 34800 bp in length
53508 53607: gap of 100 bp
53508 97651: contig of 44044 bp in length
97652 97751: gap of 100 bp
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1 38476 c 39574 g
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/clone_lib="RPCI-11 Human Male BAC"
1. .18607
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/db_xref="taxon:9606"
/chromosome="3"
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184321: contig of 86570 bp in length
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Pred. No. 4.
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to mRNA, clone_lib:MAMMA1
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BASE COUNT
ORIGIN
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AF387518/c
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                                                                                                             REFERENCE
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                                                                                                                                                                                                                                                                                                                  VERSION
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TITLE
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Best Local
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                                                            TITLE
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         JOURNAL
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Direct Submission

Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Submitted (10-MAY-2001) Takao Isogai, Kisarazu, Chiba 292-0812, Japan
(B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of
Bconomy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology, cDNA library construction,
5'-& 3'-end one pass sequencing and clone selection: Helix
Research Institute (supported by Japan Key Technology Certer etc.)
and Department of Virology, Institute of Medical Science,
Instruction of Technology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster Rho-GTPase activating complete cds.
                                 L (bases 1 to 4695)
Billuart, P., Winter, C.G., Maresh, A., Zhao, X. and Luo, L.
Billuart, P., Winter, C.G., Maresh, A., Theo, X. and Luo, L.
Billuart, P., Winter, C.G., Maresh, A., Zhao, X. and Luo, L.
Billuart, P., Winter, C.G., Maresh, A., Zhao, X. and Luo, L.
                                                                                                                                        Drosophila melanogaster.
Drosophila melanogaster.
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
Regulating axon branch stability: the rol repressing a retraction signaling pathway Cell 107 (2), 195-207 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Tokyo.
                                                                                                                                                                                                                                                                                                               AF387518.1 GI:15553436
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IGDRSVSLIVFILDGKPTVGZTHTIKININRRAAGGVCIFTIGIGDNOPERLIEKI.
SLENGGITRRAHEEEDAGSQLIGFYDEIRTIKINDRPERAAGGVCIFTIGIGSVDGATKILEFAVEN
GSEIIIAGKLVDRKLDHLHVEVTASNSKKFIIIKTDVPVRPQKAGKDVTGSFRPGGDG
GGDRHIERLMSTLTTKELLSSWLQSDDEFEKERLKQRAQALAVSTREIFFTSHKIRK
GFVFRMOGLEBAHGKSAAMGPEFVYOSVTGAGTOFDLIKKFVQPIKISKTSVDGDP
HFVVDFPLSRLTVCFNIDGQPGDIIRLVSDHRDSGVTVNGELIGARAPPNHKKQRTY
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gdkyvoceiterekksgdpykekknyteenveksteifase
ellorrigkyenistoyrocysistenveksteiste
ellorrigkyenisteaniiekptyvoortnidesdiiktdyneeostoyl
dsgppostyinometeaniiekptyvoortnandistetilhdlepodresii
ngtfyhytapkolpplpknyvfyldssasmystklrotkdalftilhdlepodresii
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/clone="MAMMA1000897"
/tissue_type="mammary gland"
/clone_lib="MAMMA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIQGSIAFVILIHLYKKPAPFQRHHLGFYIANSEGLSSNCHGLLGQFLNQDARLTEDP
AGPSQNLTHPLLLQVGEGPEAVLTVKGHQVPVVWKQRKIYNGEEQIDCWFARNNAAKI
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/db_xref="GI:14042009"
/translation="MilliglclclclslcvgsqebAgswgHsseqbglrvprqvrligr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="unnamed protein product"
/codon_start=1
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94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                              protein
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in p190 mRNA,
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                   DEFINITION ACCESSION
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AY121666/c
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                                                                                                                                                                                          SOURCE
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TITLE
JOURNAL
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Best Local
                                                                                                                                                           ORGANISM
                                 AUTHORS
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prosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 5878)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise
                                                                                                                                                                                                             AY121666.1
FLI_CDNA.
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AY121666
                                                                                                                                                                                                                                                                                                                      AY121666
                                                                                                                                                                                          fruit fly.
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EVRYLEWGREGFEALSEHDCQQIYDIHQDDIIEKSKOINFVELLLHAQYFLQFKNYDN
ITQBDVRG1TDVIQBDSKYKMLDBLDQERKALVQHLAFHQYFLGFENVONSL
IEBYLSDKSASNHKTPSGGGWKSSGSGSDRTLNLLIVGSEHLASDLLNDIRICTGSKG
EYIYENQOYYLNYKIANGKOMEAFKALDVYSSGLICVYSNQCSFETIKDNLERTLCNL
ELBDKFERKLFYLVYQDQDLKENEVEYLINGBGGHKSSMLHCDFIDHTQNHLKTYLDLI
NIVILSLKLTENKSYEPIPSNHTDLRILCCIPGGDYDIBNIVQPLVEESTLVKANEH
SIIYUDFFIGDAKRKYEFILSSYHGTSQYKDELHGYIYYTGKRKSSLANLSIIAAQN
ANIPLQIIAVPSGGTVNAFFNSDLOGFLITEGONVADREKGSFWIESKJCSTGTDF
SGSENYEMAYTGKRHIDSNLNKLTRKGSFGOTLKVSHADREKGSFWIESKDSRCHMKNLLI
WNAFSGSTHAYTTGKRHIDSNLNKLTRKGSFGOTLKVCEAFSSNCFMASSTFTLFVQ
PGELINMKNEDLYSDAYAKMETGGSGSGSGSGSGSGSGTGLGLGSGSGCMGDSFLEBY
PGELINMKNEDLYSDAYAKMETGGSGSGSGSGSGSGSGTGLGLGSGSGCMGDSFLEBY
PGELINMKNEDLYSDAYAKMETGGSGSGSGSGSGSGSGTGLGLGSGSGCMGDSFLEBY
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NRSVEKQVEFVQNVIATILKNKKPLVLVTTKNDDATELJVREAEKISQRKDYKSTVQL
IETSAHESINIDLAFLLLAQMIDKVKNRVKIISYQESAKSRKELLDFESEAVTRLIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Rho-GIPase activating protein p190"
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/db_xref="G1:11553457"
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KKPVAAKKQKKKKVAIPVQTPRVPPFGSYVSPPEIPLHYQRMAVGGSGPGEKKKPEPC
VPEPMKSDKSPEYSMVPELAGAGIFGAENLPFYNNKQAKCIKDEKLEKRRIKEETAR
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DKFALALEYLLPDIGALNISDDDAWECARNYLQNHIEFEQYFFECPQASWTELVDMDE
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/db_xref="taxon:7227"
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LFSKDIIKELEEIAGSRGVGNSKLNVEVKTDRSCRLIALKSLLQKLPPINFAIIKYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRKLQEKEKEQEKKLKRKLKQNAKGLVESAEAQFGKLMITSEQGEIPIFLNKCVEFIE
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Pred. No. 7.
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Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-JUN-2002) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, Ca 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
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    1595
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EVWVLFYGGREGFEALSEHGCQQITDIRQDDIIEKSKORWYGELLEHAQYELGFKYUN
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PGKLNMKNEQLYSJAYKNNFTGSGSGSGSGSGSTGLGLGLGSGSGRRNKGNSFTELPTQQ
PGKLNMKNEQLYSJAYKNNFTGSGSGSGSGSGSGTGLGLGSGSGRRNYKAS.
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QITDYHVLWSQGSKMLSQYREWNEFLNIFGHEAGQKLFRRHMKKLRDDHLNKKLHQYL
DKFALALEYLLFDIGALNISDGDAWECARNYLQNHIEFEQYFFECPQASWTELVDMDE
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MDFYSKRCTATKVFSAEKLMYICKNQLGIEKEYEQKVMPDGRLSIDGFVVVFDVSSYV
NRSVEKQVEFVQNVIATILKNKKPLVLYTTKNDDAYELIVARAEKISQRKDYKSTVQL
                                                                                                                                                                                                                                               KKEVAAKKQKKKKVAIPVQIPRVPPEGSYVSPPEIPLHYQRMAVGGSGPEKPEPCVPE
FMKSDKSPEYSMVPELAGAGIFGAENLPEYNMNQAKCLKDFEKLEKRRIKEETARQRK
                                                                                                                                                               LDSEGIYRVPGSRAHVDMLFQRFEEDTNTEIDALDIPVNAVATALKDFFSKRLPPLFS
                                                                                                                                                                                                           LQEKEKEQEKKLKRKLKQNAKGLYESAEAQFGKLMITSEQGEIPIFLNKCYEFIEKEG
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/db_xref="GI:21464380"
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/strain="y; cn bw sp"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete genome.
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17; Conser
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LDVYGLISATAIDPIEKKPLTHFYPGALVLSFSTFGCNWACQYCQNFEISQRRRAEGF
EVTPELLVKWAESYGAHGITYTYNEPTIFMEFAHDVGVLAKSKGLFNTFVTNGYMTPE
AVKYASEFLDAATYDFKGNADEKFMRKYIYVPDAEPIFETLAEMKRYGINVEVTDLVV
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366. .1457
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/gene="PAE3183"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(118. .231)
/gene="PAE3183"
                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein_id="AAL64733.1"
/db_xref="GI:18161451"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism≈"Pyrobaculum
/strain="IM2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                 /protein_id="AA164734.1"
/db_xref="GI:18161452"
/translation="MEAVLSRALPDGRVECTACARRCKLREGQTGFCGVRTVRGGRLV
                                                                                                                                                                                       /gene="PAE3184"
                                                                                                                                                                                                                                                                         /product="sRNA,
                                                                                                                                                                                                                                                                                         /gene="PAEsR34"
                                                                                                                                                                                                                                                                                                                       gene="PAEsR34"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:13773"
                                                                                                                   product="pyruvate"
                                                                                                                                   transl_table=11
                                                                                                                                                       codon_start=1/
                                                                                                                                                                     'note="Protein fate;
                                                                                                                                                                                                                                                                                                                                                           translation="MPLESPALLSSKRVKLGVFGTEELCGGDVSYCVGVSG"
                                                                                                                                                                                                                                                                                                                                                                                                                                transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="Hypothetical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .14086
                                                                                                                                                                                                                                    ...uuru="skNA, predicted to direct ribose methylation of .13 (lys) at G10" .1457
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94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16.4;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain
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strain IM2 section 171 of 201
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                                                                                                                   formate-lyase
                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aerophilum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 3;
7.2e+02;
mes 1;
                                                                                                                                                                     modification and repair"
                                                                                                                     activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5878;
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L of the
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3475...4131
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2794. .3171
                                                                                                                                                                                complement(5555. .5728)
/gene="PAE3192"
                                                                                                                                                                                                                            complement(5555.
/gene="PAE3192"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(4852. .5523)
/gene="PAE3189"
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/gene="PAE3189"
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4131. .4895
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EGARFAYVGNVPGHRYEHTYCPECGRVVIKRRGFDILEINLYEKGGEYRCKFCGAKIP
                                                                                                                                                                                                                                                                                                                  /translation="MPFSYGELLISWLGHDSFRITGGGFVLYIDPYGLQVGDPKADAI
LITHEHFDHCDPPSIGRILKPSTVVVAPRVARQCALKAARNVABISPGEEREVGPLKI
RAFPAYNINKFRDPARGVVFHPKEDGRVAYLIEWGGVRIFHAGDSDFVPEFREVRADV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MELYGLILAALLIYNNSLYLLGPTAWGAGIGARKAFVIAAAAQL
LGVIJSYMAQLFISLPEFLYIGAAYLLLSLVXISLPISVIGYSHAPEBAVALWILS
PLYSVATVALCKTLKRGRPLAALSLFLVMXLFGFNAVALFTRAALAAAVVAGTYFG
LGESRWVIDIAALRKTAAAVNLTVALGALAGILLSVPISFTLVAYSSILAASYSQGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4131. .4895
/gene="PAE3188"
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AKEIRRGRHLWTNDAIYSIYSAELKEMLDLYRTMLEYLQTMIKTNKAEDLRRYARIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="conserved hypothetical protein"
/protein_id="AAL64736.1"
/db_xref="GI:18161454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="PAE3187"
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LSIAVRLKRLLPKPYDVRAAAYAVARALAMAKYVABKCRDSPTWKVKTWELKMAVEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKGKIMPTWRDEFRFVYVPIQTFARWVRR"
                                                                                                                                                                                                                                                                                                                                                                                    /product="conserved hypothetical protein"
/protein_id="AAL64738.1"
/db_xref="GI:18161456"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
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/db_xref="GI:18161455"
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/protein_id="AAL64735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Hypothetical; Conserved within genome"
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/protein_id="sal64739.1"
/db_xref="G1:18161457"
translation="MSKKQKLKFYDIKAKQAFETDQYEVIEKQTARGPMMFAVAKSPY
                                                                                                                                                                                                                                                                                                 /LVPVSGVYVMTPQEAAEFVNAVMPKVAIPMHYGSIVASRREAEEFKRLVRPEVQVVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Hypothetical; Conserved"
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                                                                                                           'transl_table~11
                                                                                                                                      'note="Hypothetical; Conserved"
'codon_start=1
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Best Local
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                                                                       Conservative
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6254. .6838
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5923. .6342
                                                                                                                                                                           LERLEDSNYRDNYVRWPIPYRLLELAMTLPAGGCRILGREVRTKKRGVARVERELYC"
complement(8131..10143)
/gene="PAE3197"
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/db_xref="G:18161461"
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/translation="MGVEICRSLLECLGALGRSQREDSAALTREWGEAKRANE
RLAGVULIRGBARPLADMENRLWARALFTEDVALWEGEGGDLPENCAARATGVSAKALLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MALILAAIVAVAYAVLAPLLFPAVVLTQAALGIKDYITAFAVLA
AVSAAAMYIISPYIINAVFGPRFDPGLQQLVDAVAAKLGGRVKARAVVVEGPPKRLRL
RQLPNGEYRGGDHGLVKHGEPRRAGGRHRPRAGTPHK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tanalation="Mavitgliavraspoelbavighetinkompintaliotipsi
Apptgvaaihe(eldadrerspilaiayevmivvspyvvyvspyspyrapyrabyraboede
Argkdammralakiihkyyaqonpbalatspkisgekalpiyalinaaanpliditpeev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Cellular processes; conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="possible heat shock
1, authentic frameshift"
/protein_id="AAL64741.1"
/db_xref="GI:18161459"
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/protein_id="AAL64740.1"
/db_xref="GI:18161458"
                                                                                                                                                          complement(8131.
                                                                                                                                                                                                                                                     PPSAVLAGHYVCWARALAARLLEGKVGRLDSGMEAYEAAVQAGAESCWGEAKRAAEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="PAE3196"
7139. .8140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2, authentic frameshift"
/protein_id="AAL64742.1"
/db_xref="GI:18161460"
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/transl_table=11
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/transl_table=11
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/note="Cellular |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="possible heat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Hypothetical"
                                                                                        82.0%;
94.4%;
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Pred. No. 7
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                                                                                                                                                            .10143)
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TITLE
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Best Local
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Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CDM:10210776 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'Working draft' sequence.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clasiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K.,
                                                                                                                                                               Celniker, S.E. Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, Butenhoff, C., Champe, M., Chavez, C., Chew, M., Cieściolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, J.K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 40123)
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoá; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophildae; Drosophila.

1 (bases 1 to 65961)
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                                                                                                                                               Sequencing of Drosophila melanogaster
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SOURCE VERSION

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in length

ORIGIN

FEATURES

COMMENT

SOURCE

Submitted (02-DEC-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contlys in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draff' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is anotherary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Syirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M. as soon as it is available and the accession number will be preserved. 5716 5798 6596 6596 6596 6596 8286 8286 8286 8286 8286 8286 8286 10372 111317 1 3445 4010 4090 4785 1814 2419 2499 Submission 10451 16458: 15130: 6: gap of unknown length
6: contig of 990 bp in length
6: gap of unknown length
1: contig of 745 bp in length
1: gap of unknown length
1: gap of unknown length
1: gap of unknown length
0: contig of 6140 bp in length
0: contig of 619 bp in length 5: gap of unknown length
4: contig of 669 bp in length
4: gap of unknown length
11: contig of 1337 bp in length
12: gap of unknown length
13: gap of unknown length
14: gap of 185 bp in length gap of unknown length contig of 1328 bp in 1 gap of unknown length contig of 1457 bp in 1 gap of unknown length contig of 1160 bp in 1 gap of unknown length contig of 1748 bp in 1 gap of unknown length contig of 1516 bp in 1 gap of unknown length contig of 671 bp in 1 gap of unknown length contig of 671 bp in 1 gap of unknown length contig of 671 bp in 1 gap of unknown length contig of 671 bp in 1 gap of unknown length contig of 1482 bp in 1 gap of unknown length contig of 1676 bp in 1 gap of unknown length contig of 724 bp in 1 gap of unknown length contig of 806 bp in 1 gap of unknown length conting of 695 bp in let gap of unknown length conting of 853 bp in let gap of unknown length conting of 718 bp in let gap of contig gap of contig gap of unknown lengum contig of 605 bp in le gap of unknown contig of 997 k contig of 656 bp in length of 718 bp in lenging of 718 bp in length of unknown league ig of 866 bp in len ig on length in le ig of 806 bp in length g of 565 bp in Les unknown length of 1289 bp in 10 tunknown length of 671 bp in le unknown of 1527 997 bp in length bp in length
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                                                                        Rubin G.M.

Burect Submission

Direct Submission

Submitted (02-NOV-1999) Drosophila Genome Center, Lawrence Berkeley

Laboratory, Ms 64-121, Berkeley, CA 94720, USA

On Nov 4, 1999 this sequence version replaced 91:6175114.

For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruiffly.or/sequence/) or send email

to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet

* NOTE: This is a 'working draft' sequence. It currently

* consists of 101 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kearney,L., Lee,B., Lewis,S., Li,P., Ling,H., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfelifer,B., Richards,S., Sethi,H., Svirskas,R.R., Wan,K.H., Webster,D., Woolley,P., Yang,S., Yee,M., Yu,C. and Rubin,G.M. Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute Drosophila melanogaster BAC library, partial EcoRI pBACe3.6"
a 14437 c 13716 g 16689 t 4727 others
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94.4%;
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         contig of 577 bp in length; gap of unknown length; contig of 747 bp in length; gap of unknown length; contig of 829 bp in length
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Pred. No. 7e+02;
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in length
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Karra, K.,

SEQUENCING IN HTG 04-NOV-1999 3 (D1121)

0;

Gaps

0;

in

FEATURES

source

of 768 bp in unknown length of 1055 bp in unknown length of 409 bp in unknown length of 572 bp in unknown length of 1128 bp in unknown length of 1128 bp in unknown length of 903 bp in unknown length of 636 bp in unknown length	of unknown length ig of 704 bp in length ig of 704 bp in length of unknown length in length ig of 1015 bp in length ig of 611 bp in length ig of 612 bp in length ig of 642 bp in length of unknown length ig of 842 bp in length of unknown length ig of 774 bp in length ig of 774 bp in length ig of 834 bp in length ig of 763 bp in length ig of 763 bp in length of unknown length ig of 763 bp in length ig of 103 bp in length ig of 103 bp in length ig of 103 bp in length ig of 599 bp in length ig of 599 bp in length ig of 875 bp in length in length ig of 875 bp in length ig	if unknown length g of 738 bp in length if unknown length g of 508 bp in length g of 508 bp in length if unknown length if unknown length g of 822 bp in length g of 590 bp in length g of 682 bp in length g of 680 bp in length if unknown length g of 964 bp in length g of 645 bp in length g of 616 bp in length g of 683 bp in length g of 804 bp in length g of 804 bp in length g of 805 bp in length g of 806 bp in length in unknown length g of 806 bp in length in g of 685 bp in length in g of 708 bp in length in g of 708 bp in length in g of 610 bp in length in length in g of 610 bp in length
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	Query Match Best Local Similarity 94.4%; Pred. No. 7e+02; Matches 17; Conservative 0; Mismatches 1 QY 3 ATTRACGCCCACGCTCTC 20
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Helicobacter pylor	AAS53662	23	2577		•	4
	AAF25651	22	2577	•	•	ũ
H. pylori cytoplas	AAT67908	18	2547	•	•	ວ
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H. pylori cytoplas	AAT67489	18	336			õ
Chemically treated	ABL70604	24	34548	•	•	ĕ
Human angiogenesis	ABQ67006	24	33053			8
Signal transductio	ABK31213	24	19459	79.0	15.8	7
Chemically treated	ABL70528	24	19459	•	•	ŏ
chemically	ABN80049	24	9543		•	ŭ
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Human immune syste	ABL32860	24	7631	•	٠	ũ
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Ω,	ABL70379	24	6922	•		õ
Tumour suppressor	AAS46533	22	6922	•		io
cally p	AAS63341	24	6207			œ
	ABL33551	24	6075	•		7
	ABL05750	23	6020		٠	'n
_	ABL05751	23	3759	•	•	Ċī
Oligonucleotide fo	ABQ34483	24	890	•	•	4
ide	ABQ34482	24	890	•		w
encoding nove	7581	23	729	79.0	•	Ö
Ħ	8999	23	729	•	•	i
Drosophila melanog	ABL13874	23	5484	82.0	16.4	0

ALIGNMENTS

Schistosoma mansoni repeater unit 3' PCR primer.

Schistosomiasis; infection; diagnosis; PCR primer; ss

07-JAN-2002 AAI70402;

(first entry)

AAI70402 standard; DNA;

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RESULT 1
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biagnosing infection by parasites of the Schistosoma sp. in a biological sample especially useful in cases of low infection intensity, comprises detecting a specific region of the DNA of schistosoma by polymerase chain reaction -Teles Rabello AL, 04-APR-2000; 2000BR-0001536 04-APR-2001; 2001WO-BR00035 11-OCT-2001. WO200175148-A1 Schistosoma mansoni. (FIOC-) FIOCRUZ FUNDACAO CRUZ OSWALDO. 2001-648561/74. Dias Neto E, Pontes F

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AAI70400/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of a claimed oligonucleotide primer, derived from the 3' region of a highly repeated short DNA sequence (see AAI70400) of the Schistosoma mansoni genome. This 3' primer, and the 5' primer given in AAI70401, are used in the method of the collection of diagnosing Schistosoma infection. The method involves collection of the sample to be examined, extraction of Schistosoma sp. DNA, amplification by PCR, separation of PCR products by electrophoresis, and detection e.g. by colouring with silver salts. A kit for diagnosing infection, which includes the primers, is claimed. The method is useful for detecting Schistosoma sp. Claimed. The method is useful for detecting Schistosoma sp. Claimed. The method is useful for detecting Schistosoma sp. the parasites by detecting the parasite's DNA in a biological sample. It is especially useful in cases of low infection intensity for which parasitological stool tests demonstrate little sensitivity.
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Best Local
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                                                                 Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schistosoma mansoni repeater unit DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI70400 standard;
                                                                                                               Schistosoma
                                                                                                                                Diagnosing infection by parasites of the Schistosoma sp. in a biological sample especially useful in cases of low infection intensity, comprises detecting a specific region of the DNA of
                                                                                                                                                                                                                               WPI; 2001-648561/74.
                                                                                                                                                                                                                                                                           Teles Rabello AL,
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/*tag=
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                                                                                                               reaction
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sequence

ent sequence is that of a highly repeated short DNA in the genome of Schistosoma mansoni. PCR primers

such as hormone deficiencies,

metabolic deficiencies,

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Matches
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             recombinant vector. This sequence contains the green fluorescent protein (GFP) coding sequence from Aeguorea victoria, and the SM1-7 coding sequence from Schistosoma, along with promoter sequences. The invention relates to a eukaryotic diploid multicellular parasite transformed with a transgene. Transgenic eukaryotic parasites are useful as universal grafts for in vivo delivery of beneficial gene product in humans and animals. The parasites can particularly be used for restoration of deficiencies whether acquired or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            universal graft; transgenic eukaryotic parasite; acquired deficiency; genetic deficiency; hormone deficiency; metabolic deficiency; hamatological deficiency; immunological deficiency; immunological deficiency; immunological deficiency; anti-microbial therapy; anti-cancer therapy; drug addiction; poisoning condition; geriatric condition; ds.
                                                                                                                                            This sequence represents a GFP-Sm1-7 fusion
                                                                                                                                                                                                        Eukaryotic diploid multicellular parasite useful as universal grafts for in vivo delivery of beneficial gene products in humans and animals involves transformation with a transgene
                                                                                                                                                                                                                                                                                                         Hamburger J,
                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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glutathione S-transferase; eukaryotic diploid multicellular para
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFP-Sm1-7 fusion protein construct.
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                                                                                                                                                                            Fig 6; 90pp; English.
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                                                                                                                                                                                                                                                                                                         Laban A;
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                                                                                                                                                                                                                                                                                                                                                                                                       99WO-IL00651.
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                                                                                                                                               construct
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                                                                                                                  fluorescent protein
                                                                                                                                               contained within
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CC This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method CC is used: (i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory cosystems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide for detecting cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   haematological deficiencies, immunological deficiencies, immunotherapy, anti-microbial therapy, anti-cancer therapy. They can also be used for
                                                                                                                                                                                                                                                                                                                                                         Determining the degree of for diagnosis and prognosi
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-371829/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2001; 2001WO-EP10074.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutagenesis and malignant transformation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Piepenbrock C,
                                                                                                                                                                                                                                                                                                                             ...y the degree of cytosine methylation in genomic DNA, osis and prognosis, comprises selective hybridization from chemically treated DNA -
                                                                                                                                                                                                                                                                                                    56pp + Sequence Listing; 56pp; German
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Pred. No.
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of
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This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method CC is used: (i) for diagnosis and/or prognosis of side effects of CC classes of oligomers, the degree of methylation is calculated. The method CC is used: (i) for diagnosis and/or prognosis of side effects of CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC of the central nervous, cardiovascular, gastrointestinal and respiratory cystems etc., particularly by detecting mutations or single nucleotide CC types and for investigating cell differentiation. The method allows the method for investigating cell differentiation. The method allows the method for determining the degree of cytosine methylation described in method for determining the degree of cytosine methylation described in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                               Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olek A,
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                                                                                                                                                                                                                                                                                                                                                                            Claim 12; 56pp + Sequence Listing; 56pp;
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18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPIGENOMICS AG
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2000DE-1044543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for detecting cytosine methylation SEQ ID NO 8660.
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the disclosure of the invention.

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CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to wracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two Classes of oligomers, the degree of methylation is calculated. The method CC is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC of the central nervous, cardiovascular, gastrointestinal and respiratory constructions (SNP's), and (ii) for differentiation of cell or tissue CC methylation status of many C residues to be determined simultaneously. DABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the CC method for determining the degree of cytosine methylation described in vex
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Best Local
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05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; con all ifferentiations.
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                                                                                                                                                                                                                                                                                                                                                                                    Claim 12;
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18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin
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Pred. No. 2
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Sequence 748

BP;

104 A; 101 C; 282 G; 261 T; 0 other;

Query Match Best Local Similarity

84.0%; 90.0%;

Score 16.8; Pred. No. 28;

DB

24; Length 748;

Sequence

B₽;

261

A; 282 C; 101 G; 104 T; 0 other;

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ABQ53095
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                                          This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-Cpc-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC plot that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one commit could be applicable of hybridisation to both classes is determined from the classe of hybridisation to both classes is determined from the classes of high pridisation to both classes is determined from the classes of cligomers, the degree of methylation is calculated. The method cis used: (1) for diagnosis and/or proprosis of side effects of the rappeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the method of the control of the degree of cytosine methylation described in
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide for detecting cytosine methylation SEQ ID
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                                   the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG~) EPIGENOMICS AG.
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Pred. No. 28;
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RESULT 8
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                    the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are primers allow obtaining of the full-length cDNAs are main of acid sequences; AAB92446 to AAB18383 to AAH18742 represent human amino acid sequences; and AAH13629 to AAH18632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                             sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                              of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID 18513; 2537pp + CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sugiyama
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; 99JP-0300253.
; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
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T, Wakamatsu A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saito K,
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RESULT 1
ABL13874
ID ABL1
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                                                                                        В
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Query Match

82.0%;

Score 16.4;

DB 22; Length 3226;

ABL13874;

ABL13874 standard; cDNA; 5484

ΒP

2810

ATTAACGCCCCCGCTCTC

2793

10

Sequence 3226 BP;

785 A; 894 C; 902 G; 645 T; 0 other;

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ARESULT 9
ABL13875/c
ID ABL1388
XX
ABL138 XX
ABL138 XX
DY 26-MAR
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DY 26-MAR
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DY DOSOP
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DY DOSOP
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DY DOSOP
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DY WO2001
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DY 27-SEP
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DY 23-MAR
PR 23-MAR
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YZ
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                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIJ6176 ABIJ6175) and the encoded proteins
                                                                                                                                                                                      Sequence 3251 BP; 849 A; 820 C; 880 G; 702 T; 0 other;
                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL13875 standard; cDNA; 3251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 36107; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster expressed polynucleotide SEQ
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                                                                                                                                                                                                                                                                                                                           (ABB57737-ABB72072)
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ATTAACGCCCACGCTCTC 20
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DB; ABB69772.
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                                                                            l Similarity 94.4
17; Conservative
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                                                                                                      82.0%;
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                                                                                                      Score 16.4; D
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                                                                               Pred. No. 53;
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                                                                                                                                     3251;
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RESULT 11
AAS66682/c
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                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLO1840-ABL16175) and the encoded proteins (ABBC7737-ABB72072).
                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                           Sequence 5484 BP; 1402 A; 1280 C; 1322 G; 1480 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
11-OCT-2001.
                        WO200175067-A2
                                                 Homo sapiens
                                                                                                                                         13-FEB-2002
                                                                                                                                                                                          AAS66682 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US09231
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                                                                                                             DNA encoding novel human diagnostic protein #2486
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                                                                                                                                                                                                                                                         652 ATTAACGCCCCCGCTCTC 669
                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                 3 ATTAACGCCCACGCTCTC 20
                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                           l Similarity
17; Conserv
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                                                                                                                                                                                                                                                                                                           Conservative
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2000US-0614150.
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                                                                                                                                                                                          cDNA;
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94.4%;
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Pred. No. 56
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RESULT 12
AAS75819/c
ID AAS75819;
XX AAS75819;
XX AAS75819;
XX AAS75819;
XX DY 13-FEB-2002 (first e
XX DY DNA encoding novel he
XX DY Encoding novel he
XX Human; chromosome maj
XX Homo sapienent; medi
XX PM W0200175067-A2.
XX PM W0200175067-A2.
XX PF 30-MAR-2001; 2001WO-1
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The sequence data for this patent did not appear in the printed consistic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
 30-MAR-2001; 2001WO-US08631.
                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                               DNA encoding novel human diagnostic protein #11623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 2486; 103pp; English.
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
17; Conserv
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                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 269 A; 175 C; 148 G; 137 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  relates to isolated
                                                                                                                                                                                                                                                                                                          cDNA;
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ABQ34482/c
ID ABQ344
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CC Note: The sequence data for this patent did not appear in the printed company of the product of the printed company of the product of the printed company of the product of the printed company of 
01-SEP-2001; 2001WO-EP10074.
                                             07-MAR-2002.
                                                                                                                                    Homo sapiens
                                                                                                                                                                                                           gastrointestinal; respiratory system; single nucleotide
                                                                                                                                                                                                                              drug; side effect; cancer; central
                                                                                                                                                                                                                                                 Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                                                                                                                                                  Oligonucleotide for detecting cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ34482 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 729 BP; 269 A; 175 C; 148 G; 137 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 11623; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT,
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YT;
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Pred. No. 94
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                                                                                                                                                                                                                                nervous system;
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01-SEP-2000; 2000DE-1043826
05-SEP-2000; 2000DE-1044543
                                                                                                                                                                                 Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                    Oligonucleotide for detecting cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 890 BP; 134 A; 106 C; 283 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA -
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05-SEP-2000; 2000DE-1044543.
                                               01-SEP-2001; 2001WO-EP10074.
                                                                                                                                                                                                                                                                                                     12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                         ABQ34483 standard; DNA; 890
                                                                                                                 WO200218632-A2
                                                                                                                                                  Homo sapiens.
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Pred. No 9
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RESULT 15
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Query Match
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Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SRP's): and (il) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. BaQ1310-BaQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligoners, the degree of methylation is calculated. The methologies of oligoners, the degree of methylation is calculated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 890 BP; 367 A; 283 C; 106 G; 134 T; 0 other;
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               Venter JC,
                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                            23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                  27-SEP-2001.
                                                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                                                                       Drosophila melanogaster.
                                                                                                                                                                                                                                                                                         pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster expressed polynucleotide SEQ ID NO 11735.
                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002 (first entry)
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                                                 (PEKE ) PE CORP NY.
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               Adams M,
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Pred. No. 96;
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Search completed: May 12, 2003, 01:14:58
Job time : 37.2143 secs

В 8

3044 TATTAACCCCCACGCTATC

3062

2 TATTAACGCCCACGCTCTC 20 l Similarity 17; Conserv

Conservative

0;

79.0%; 89.5%;

Score 15.8; DB 23 Pred. No. 1.1e+02; Mismatches

DB 23;

Length Indels

3759;

0; Gaps

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Query Match Best Local S Matches 17

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DR PHH DR PHH XXX
                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG18511), expressed DNA sequences (ABLIG1851) and the encoded proteins (ABBS7737-ABB72072).
Sequence 3759 BP; 963 A; 927 C; 946 G; 923 T; 0 other;
                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 11735; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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1: /cgn2_6/ptodata/1,
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3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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Match
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20
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Listing first 45 summaries
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     12, 2003, 01:08:23; Search time 8.78571 Seconds
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698.126 Million cell updates/sec
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/cgn2_6//todata/1/ina/5B_COMB.seq:*
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/cgn2_6//todata/1/ina/6B_COMB.seq:*
/cgn2_6//todata/1/ina/PCTUS_COMB.seq:*
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     GenCore version (c) 1993 - 2003
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  US-09-074-579-2
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US-08-673-190A-4
US-08-673-190A-6
US-08-414-926A-6
US-09-253-682-6
US-09-527-657-6
US-09-532-594B-14
US-09-532-594B-3
US-09-532-594B-1
US-08-760-489-1
US-08-760-489-3
US-09-185-373-3
US-09-185-373-3
US-09-185-373-3
US-09-185-373-3
US-09-185-373-3
US-09-185-373-9
US-08-453-594B-1
US-08-453-594B-1
US-08-453-695A-92
US-08-453-702A-92
US-08-453-702A-92
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Compugen Ltd.
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Query Match

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TELEPHUME: 050-835-055 TELEERX: 650-845-4166 TELEX: INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 3636 base pairs TYPE: nucleic acid STRANDEDNESS: single TYPE: linear IMMEDIATE SOURCE: LIBRARY: UTRSNOT02 CLONE: 688183 US-09-074-579-2	1 H C H O 2 H >	Porter Drive Lito Lito Lito Lito Lito Lito Lito Lito	RESULT 1 US-09-074-579-2/c US-09-074-579-2/c Sequence 2, Application US/09074579 Patent No. 6001596 GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L. APPLICANT: Hillman, Jennifer L. APPLICANT: Guegler, Karl J. APPLICANT: Patterson, Chandra FITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE TITLE OF INVENTION: INHIBITOR HEAVY CHAIN PRECURSOR NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Pharmaceuticals, Inc.	28 13.6 68.0 131 5 PCT-US93-12588-92 29 13.6 68.0 131 5 PCT-US95-08071-92 c 30 13.6 68.0 1117 4 US-08-858-207A-40 31 13.6 68.0 1503 4 US-09-172-952-6 c 32 13.6 68.0 1509 2 US-08-481-337A-1 c 33 13.6 68.0 1509 5 PCT-US95-05467-1 c 34 13.6 68.0 1509 5 PCT-US94-11328A-3 c 36 13.6 68.0 1556 5 PCT-US94-11328A-3 c 36 13.6 68.0 1586 5 PCT-US94-11328A-3 c 37 13.6 68.0 1588 4 US-09-9517-80-4 c 38 13.6 68.0 1588 4 US-09-9517-80-4 c 40 13.6 68.0 1584 4 US-09-352-256-1 c 41 13.6 68.0 1584 4 US-09-352-256-1 c 42 13.6 68.0 1584 4 US-09-436-265-1 c 43 13.6 68.0 1584 4 US-09-79-187-1 c 44 13.6 68.0 3663 4 US-09-06-942-25 d 45 13.6 68.0 3663 4 US-09-206-942-25 d 58 13.6 68.0 3808 2 US-08-417-210A-79
				Sequence 92, Appl Sequence 40, Appl Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli

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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 88.9
Matches 16; Conservative
                                             sequence 4, Application US/08673190A Patent No. 5985668
                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                               Matches
                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: UTRSNC
CLONE: 688183
                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Guegler, Karl J.

APPLICANT: Patterson, Chandra
TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
TITLE OF INVENTION: INHIBITOR HEAVY CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 31/-
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hillman, Jennifer L.
APPLICANT: Klein, Kathrin
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 3636 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: 000 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     660 ATATTCACGTCCACGCTC 643
                                                                                                                                    660 ATATTCACGTCCACGCTC 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                            LENGIH: 3636 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/388,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Incyte Pharmaceuticals, Inc STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                              TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATATTAACGCCCACGCTC 18
                                                                                                                                                                1 ATATTAACGCCCACGCTC 18
                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cerrone, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09388774
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                                                                                                                                                                                               Conservative
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              Mattes, Ralf
                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette
                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                            74.0%;
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                                                                                                                                                                                                            Score 14.8;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SD
                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                         Length 3636;
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RESULT 4
US-08-672-850-5
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08672850 Patent No. 6140117 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
-- Tocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: FORMAN, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 0647
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: D
ORIGINAL SOURCE:
ORGANISM: Ente
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                             ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                STREET: FOUL STREETS STREETS STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Sucrose Metabolism Mutants NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
                                                                     COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             APPLICANT: Milbrandt, Jeffrey APPLICANT: Araki, Toshiyuki TITLE OF INVENTION: NINJURIN
APPLICATION NUMBER: US/0
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Stegmaier, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: LL.
STRANDEDNESS: DULL
TOTOGY; linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 TATTGACCACCACGCTCTC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0:
FILING DATE: 27-JUN-1996
CLASSIFICATION: 435
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ZIP: 20005-3315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
)EDNESS: both
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1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : (202)408-4000
(202)408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacter species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.0%;
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                                                          US/08/672,850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.2;
Pred. No. 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 308;
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LOCATION: 1401..2384

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US-08-414-926A-6; Sequence 6, Application US/08414926A; Patent No. 5721354; GEMERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (genomic) US-08-672-850-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.0%; Score 14.2; DB 3; Length 1235; Best Local Similarity 84.2%; Pred. No. 1.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1235 base pairs
                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 18318 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1192 ACAATAAAGCCCACGCTCT 1210
                                                                                                                                                                           MOLECUL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSLELLAND.
ATTORNEY/AGENT INFORMATION:
NAME: CSET, Luann
REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: AV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-7622
TELEFAX: 415-857-0663
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/4
FILING DATE: March 31, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94306-2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 5 Palo A
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATATTAACGCCCACGCTCT 19
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                                     OTHER INFORMATION: /product =
                                                      NAME/KEY: CDS
LOCATION: 511..1281
                                                                                                                  STRAIN: Toledo
                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Cooley Godward Castro Huddleson & Tatum STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                         Human CMV
                                                                                                                                                                                                    No
                                                                                                                                                                                                                    DNA (genomic)
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ÆRR: A-63610
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FEATURE:
NAME/KEY: CDS
LOCATION: 7813..8088
OFFER INFORMATION: /product = "UL143"
                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: CDS
LOCATION: 12133..12942
OTHER INFORMATION: /product = "UL132"
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                         LOCATION: 13569..14210
OTHER INFORMATION: /product = "UL130"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: FEATURE:
FEATURE:
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                                                                     APUALE:
NAME/KEY: CDS
LOCATION: 1004..1528
LOCATION: /product =
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LOCATION: 4944..5285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 3283..3789
OTHER INFORMATION: /product == "UL138"
          NAME/KEY: CDS
LOCATION: 3063..3350
OTHER INFORMATION: /product = "UL137"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 9910..10260
OTHER INFORMATION: /pj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IOCATION: 9327..9626
OTHER INFORMATION: /product =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 8468..8995
OTHER INFORMATION: /product = "UL144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 6908..7825
OTHER INFORMATION: /product =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 5558..6832
OTHER INFORMATION: /product = "UL141"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 4355..4759
OTHER INFORMATION: /
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                                                                                                                                                NAME/KEY: CDS
LOCATION: 16216..16581
OTHER INFORMATION: /product = "UL149"
                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 11106..1
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 10328..10804
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                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /product = "UL147"
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                                                                                    "UL134"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "UL145"
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NAME/KEY: LOCATION:

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Db 15055 ATGTTAACGCCCGCGGTCT 15073
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                                                                                                                                                                                                                                                                              TELEFAX: 510-839-7810
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENCTH: 18318 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-834-1448
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STREET: /ou.
CITY: Oakland
CIATE: CA
STATE: CA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,922
FILING DATE: September 10, 1997
CLASSIFICATION: 536
                                                                                                                                                                                               STRAIN: Toledo FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
                                                         FEATURE:
                                                                                                                                                                                                                                                   ANTI-SENSE: NO ORIGINAL SOURCE:
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ADDRESSEE: Luann Cserr Attorney at Law
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COUNTRY: US
ZIP: 94610
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PPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
UMBER OF SEQUENCES: 27
LOCATION: 2478..3197
OTHER INFORMATION: /product = "UL136"
                                                                                                                                       LOCATION: 511..128
OTHER INFORMATION:
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Local Similarity 84.2%; Pred. No. 1
les 16; Conservative 0; Mismatch
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LOCATION: 17752..1
OTHER INFORMATION:
                                                                      OTHER INFORMATION:
                                                                                      NAME/KEY: CDS
LOCATION: 1401..2384
                                    NAME/KEY:
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17752..18759
                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                         /product = "UL133"
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                                                                    /product =
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                                                                    "UL135"
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FEATURE
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NAME/REY: CDS
LOCATION: 9910..10260
LOCATION: /product
NAME/KEY: CDS
LOCATION: 17752..18759
OTHER INFORMATION: /product = "UL151"
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LOCATION: 16216..1
OTHER INFORMATION:
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LOCATION: 3283..37
OTHER INFORMATION:
                                                                     OTHER INFORMATION:
                                                                                                                               LOCATION: 3063..33 OTHER INFORMATION:
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LOCATION: 1004..1528
OTHER INFORMATION: /product = "UL134"
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LOCATION: 13569..14210
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LOCATION: 12133..12942
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LOCATION: 11106..12053
OTHER INFORMATION: /pr
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LOCATION: 10328..1
OTHER INFORMATION:
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LOCATION: 9327..96
OTHER INFORMATION:
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LOCATION: 8468..8995
OTHER INFORMATION: /product = "UL144"
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OTHER INFORMATION: /product = "UL143"
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LOCATION: 6908..7825
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LOCATION: 5558..6832
OTHER INFORMATION: /product = "UL141"
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OTHER INFORMATION: /product = "UL140"
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               CDS
17752..18759
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RMATION: /product = "UL147"
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US-09-253-682-6
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Best Local S
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TELEPAX: 510-834-1448
TELEPAX: 510-839-7810
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18318 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/926,922
FILING DATE: September 10, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
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              NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
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CLASSIFICATION:
                                                                                                            OTHER INFORMATION:
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                                                     OTHER INFORMATION:
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                                                                     LOCATION:
                                                                                  NAME/KEY:
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INFORMATION: /product = "UL138"
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511..1281
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             3283..3789
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84.2%;
                                                     /product = "UL136"
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Pred. No. 1.4e+02;
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 Query Match
Best Local Similarity 84...
Matches 16; Conservative
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FEATURE:
NAME/KEY: CDS
LOCATION: 4944...528
OTHER INFORMATION:
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NAME/KEY: CDS
LOCATION: 3063..3350
OTHER INFORMATION: /pr
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NAME/KEY: CDS
LOCATION: 1004..152
OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
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LOCATION: 9910..107
OTHER INFORMATION:
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LOCATION:
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LOCATION:
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LOCATION:
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LOCATION: 8468..89
OTHER INFORMATION:
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LOCATION:
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LOCATION: 13569..14210
OTHER INFORMATION: /pro
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LOCATION: 12133..1
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 7813..8088
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LOCATION: 4355..4759
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9910..10260
~~waTION: /product = "UL146"
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9327..9626
TWANTION: /product = "UL145"
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5558..6832
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8468..8995
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1004.,1528
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11106..12053
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16216..16581
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10328..10804
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6908..7825
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17752..18759
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16337..18262
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RMATION: /product =
 71.0%; Score 14.2; DB 3;
84.2%; Pred. No. 1.4e+02;
tive 0; Mismatches 3;
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US-09-527-657-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18318 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-834-1448
TELEFAX: 510-839-7810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/926,922
FILING DATE: September 10, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Luann Cserr Attorney at Law
STREET: 750 Arimo Avenue
CITY: Oakland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AV
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FEATURE:
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                                   NAME/KEY:
                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/527,657 FILING DATE: 17-Mar-2000 CLASSIFICATION: <unknown>
                 OTHER INFORMATION:
                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 1401..2384
                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 511..1281
                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human CMV
STRAIN: Toledo
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                                                                                       OTHER INFORMATION;
                                                                                                       NAME/KEY: CDS
LOCATION: 3283..3789
                                                                                                                                                                 OTHER INFORMATION:
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                                 CDS
4355..4759
                                                                                                                                                                                 CDS
2478..3197
                                                                                                                                                               /product =
                                                                                                                                                                                                                                                                                                             /product = "UL133"
                 /product = "UL139"
                                                                                       /product
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                                                                                                                                                                   "UL136"
                                                                                                                                                                                                                                       "UL135"
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LOCATION: 17752..18759
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OTHER INFORMATION: /product =
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-527-657-6
                       Qy
Db 15055 ATGTTAACGCCCGCGGTCT 15073
                                                     Matches
                                                               Query Match
Best Local
                          1 ATATTAACGCCCACGCTCT 19
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NAME/KEY:
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                                                   1 Similarity
16; Conserv
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LOCATION:
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LOCATION:
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LOCATION:
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LOCATION:
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LOCATION: 13569..14210
OTHER INFORMATION: /pro
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LOCATION: 10328..10804
OTHER INFORMATION: /product = "UL147"
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LOCATION: 846
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LOCATION: 7813..8088
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LOCATION: 5558..6832
OTHER INFORMATION: /product =
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LOCATION: 1004..1528
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                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 16337...18262
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                                                      Conservative
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: 9910..10260
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9327..9626
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6908..7825
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3063..3350
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16216..16581
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                                                                  71.0%;
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                                                                Score 14.2; DB 4;
Pred. No. 1.4e+02;
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                                                      Mismatches
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                                                                              Length 18318;
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Gaps

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US-09-134-078-4
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US-09-532-594B-14/c
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                                                                                                                             GENERAL INFORMATION:
APPLICANT: Chorini, John A.
                                                                                                                                                             Sequence 14, Application US/09532594B Patent No. 6468524
                                                                                                                                                                                                                                                                                                                             Matches
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                                                                               APPLICANT: APPLICANT:
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APPLICANT: Davidson, Beverly TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF FILE REFERENCE: 14014.0252U2 CURRENT APPLICATION NUMBER: US/09/532,594B CURRENT FILING DATE: 2000-03-22 NUMBER OF SEQ ID NOS: 22
                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1530 base pairs
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TELEPHONE: 858/677-1456
TELEFAX: 858/677-1465
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bylina, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                               727
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                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/056,916 FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                            Kotin, Robert M.
Safer, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Gray Cary Ware & Freidenrich LLP 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: Windows95
FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                           69.0%;
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                                                                                                                                                                                                                                                                                                                                            Score 13.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                        Length 1530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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; OTHER INFORMATION: AAV4 Rep 68 gene US-09-532-594B-14
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US-09-532-594B-15/c
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TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REFERENCE: 14014.0252U2
CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 14 LENGTH: 1611
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Best Local Similarity
                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                  Sequence 15, Application US/09532594B Patent No. 6468524
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                      APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAA4 VECTOR AND USES THERBOF
FILE REFERENCE: 11014, 025207
CURRENT APPLICATION NUMBER: US,09/532,594B
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                     CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (1)...(1872)
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Safer, Brian
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88.2%;
                                       2000-03-22
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88.2%;
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Pred. No. 1
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Pred. No. 1
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; NAME/KEY: misc_feature
; OTHER INFORMATION: AAV4 Rep 78 gene
US-09-532-594B-15
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US-09-624-693A-20
                                                                                                                                                                                                                                                                                                  RESULT 14
US-08-818-070-1
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LOCATION: (13, 34, 46, 49, 51, 57, 59, 68, 69, 73, 75 - 77, 79, 82, 84,
OTHER INFORMATION: n = A or C or G or T; "n" indicates no consensus at that position
OTHER INFORMATION: Description of Artificial Sequence: Consensus
OTHER INFORMATION: Sequence of SEQ ID NOS: 12, 16, and 18
Patent No. 6355468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/624,693A CURRENT FILING DATE: 2000-07-24 NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 2475
                                                                                                                                                                                                                                                     Sequence 1, Application US/08818070
Patent No. 5831019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Yoshida, Roberta
APPLICANT: Kootstra, Anna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Appli
Patent No. 6355468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 15
LENGTH: 1872
                                                                                                                            GENERAL INFORMATION:
APPLICANT: Tully, Timothy
APPLICANT: Bolwig, Gert M.
TITLE OF INVENTION: ASSOCIATIVE LEARNING AND THE linotte
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kootstra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polynucleotide Sequences and Methods of Obtaining and
TITLE OF INVENTION: Using Same
FILE REFERENCE: 29479/500NSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence; No. 6468524e = OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                  1162 ATTCACGCCCACGCNGTC 1179
                                                                                                          CORRESPONDENCE ADDRESS:
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    COUNTRY:
                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 TTAACGCCCACGCTCTC 20
                                             Lexington
Massachusetts
USA
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                                                               E: HAMILTON, BROOK,
Two Militia Drive
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83.3%;
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88.2%;
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Pred. No. 1.9e+02;
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Pred. No. 1.8e+02;
                                                                                      SMITH & REYNOLDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-818-070-1
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US-08-723-585-1
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Best Local Similarity
Thehes 15; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Applic
Patent No. 5831057
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Tully, Timothy
APPLICANT: Bolwig, Gert M.
TITLE OF INVENTION: ASSOCI
TITLE OF INVENTION: GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 08/723,585
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/818,070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02173
COMPUTER READABLE FORM:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL95-03pA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                   STREET: Two _
CTTY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           803 TTAAGCCCCACGCTCTC 819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                         FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 TTAACGCCCACGCTCTC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                              APPLICATION NUMBER: US/08/723,585
                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08723585
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Pred. No. 1
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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               nucleic search, using sw model
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Match
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Gapop 10.0 , Gapext 1.0
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                                                           /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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          В
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     10 US-09-878-574-857

US-09-918-995-37010

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10 US-09-820-893-43

US-09-820-893-43

US-09-918-545-64

US-09-918-545-120

US-09-918-545-120

US-09-918-876-40

US-09-918-676-40

US-09-944-413-54

US-09-944-413-54

US-09-944-403-54

US-09-944-944-54
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US-09-815-242-7299
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Sequence 7400, Apsequence 857, Appl Sequence 857, Appl Sequence 40, Appl Sequence 64, Appl Sequence 120, Appl Sequence 120, Appl Sequence 140, Appl Sequence 140, Appl Sequence 140, Appl Sequence 150, Appl Sequence 150, Appl Sequence 150, Appl Sequence 54, Appl Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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-10-176-987-5	-176-985-5	-10-176-750-5	-10-176-747-5	-10-176-492-5	-10-176-488-5	-10-175-743-5	0-175-740-5	-10-175-739-5	-10-174-588-5	-10-174-582-5	-10-174-579-5	-10-174-572-5	0-173-700-5	:-10-180-557-5	80-552-5	0-176-913-	76-757-5	0-176-482-5	75-752-5	-10-175-738-	73-706-5	0-175-737-5	176-758-5	-10-174-590-5	29-
equence 59, App	equence 59,	equence 59, App	e 59,	e 59, App	e 59,	equence 59, App	equence 59, App	e 59, App	equence 59,	equence 59, App	е 59, Арр	e 59, App	ience 59, App	e 59,	App	e 59,	gg.	59, App	59, App	e 59,	uence 59, App	e 59, App	equence 59, App	e 59, App	Sequence 54, Appl

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,7931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
; NAME/KEY: CDS
; LOCATION: (1).
US-09-815-242-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-815-242-7400/c; Sequence 7400, Application US/09815242; Patent No. US20020061569A1
                                                                                                                                                                  PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7400
LENGTH: 2535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
FILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA 011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
                                                                                                            TYPE: DNA ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr, Grant J.
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RESULT 3
US-09-878-574-857
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; LOCATION: (1)...(2577)
US-09-815-242-7299
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 2000-12-26
PRIOR APPLICATION NUMBER: 100/269,308
PRIOR BEST DESCRIPTION OF NUMBER: 100/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7299
LENGTH: 2577
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Best Local
                                                                                                                      GENERAL INFORMATION:
                                                                                                                                         Patent No. US20020110548A1
                                                                                                                                                               Sequence 857,
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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Patent No.
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                                                            APPLICANT: Byrum, Joseph R. APPLICANT: La Rosa, Thomas APPLICANT: Thompson, Micha
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                APPLICANT: Ia Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1638 ATTCACGCCCACGCTCT 1622
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                                                                                                                                                                                                                                                                                                                                       77.0%;
Local Similarity 94.1%;
es 16; Conservation
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                                                                                                                                                                                                                                                                                       3 ATTAACGCCCACGCTCT 19
                     OF INVENTION:
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5. US20020061569A1
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Zyskind, Judith W.
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Xu, H. Howard
                                                                                                                                                               Application US/09878574
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38-21(15401)B
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94.1%;
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                                                                                                                                                                                                                                                                                                                                                                   Score 15.4; DB Pred. No. 1e+02;
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CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 857
LENGTH: 382
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 37010
LENGTH: 395
                                                         PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 1529
TYPE: DNA
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Sequence 37010, Application US/09918995
Publication No. US20030073623Al
GENERAL INFORMATION:
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US-09-820-893-20/c
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; Patent No. US20020076705A1
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local Similarity 85.0%;
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Best Local &
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/531,119
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/102,895
                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/820,893
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: 31 Human Secreted Proteins
FILE REFERENCE: PX033P1
FEATURE:
NAME/KEY: SITE
                                     ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.0%;
Local Similarity 85.0%;
es 17; Conservation
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Pred. No. 1.1e+02;
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Pred. No. 1.1e+02;
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US-09-820-893-43/c
US-09-820-893-43/c
Sequence 43. Application US/09820893
Fatent No. US20020076705A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 64
Patent No. 1
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Best Local Similarity 85.0
Matches 17; Conservative
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Best Local
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/531,119
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/102,895
PRIOR FILING DATE: 1998-10-02
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TITLE OF INVENTION: 31 Human Secreted Proteins
FILE REFERENCE: PZ033P1
GIDDREN TOTAL
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CURRENT FILING DATE: 2001-11-19
CRIOR APPLICATION NUMBER: 09/148,545
PRIOR APPLICATION NUMBER: 09/148,545
                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001P1
                                                         PRIOR PRIOR
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                     PRIOR
                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1998-09-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (417)
OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1796
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||||||||||| ||| || ||||
66 ATATTAACGTCCATGTTCTC 47
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                                                                                              APPLICATION NUMBER: 60/040,161 FILING DATE: 1997-03-07
                                                                                                                                   APPLICATION NUMBER: 60/038,621 FILING DATE: 1997-03-07
                                                                                                                                                                         APPLICATION NUMBER: 60/040,333 FILING DATE: 1997-03-07
                                                                                                                                                                                                              APPLICATION NUMBER: 60/040,162 FILING DATE: 1997-03-07
                   APPLICATION NUMBER: 60/040,334 FILING DATE: 1997-03-07
                                                       APPLICATION NUMBER: 60/040,626 FILING DATE: 1997-03-07
                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   64, Application U
o. US20020164669A1
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85.0%;
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Pred. No. 1.
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Pred. No. 1.3e+02
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APPLICATION NUMBER: 60/043,568
                                   APPLICATION NUMBER: 60/
FILING DATE: 1997-04-11
                                                                                                              APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11
                                                                                                                                                                                         APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11
                                                                                                                                                                                                                              APPLICATION NUMBER: 60/043,674 FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,671
FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/043,314 FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,598
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,503
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APPLICATION NUMBER: 60/047,633
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APPLICATION NUMBER: 60/047,502
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APPLICATION NUMBER: 60/048,974 FILING DATE: 1997-06-06
                                                                          FILING DATE: 1997-04-11
                                                                                        APPLICATION NUMBER: 60/043,672
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PRIOR APPLICATION NUMBER: 60/056,908
PRIOR PILING DATE: 1997-08-22
PRIOR PPLICATION NUMBER: 60/048,964
PRIOR PPLICATION NUMBER: 60/057,650
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PRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patentin Ver. 2,0
SEQ ID NO 64
LENGTH: 2033
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US-09-148-545-64/c
US-09-148-545-64/c
; Sequence 64, Application US/09148545
; Sequence 54, Application US/09148545
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EARLIER FILING DATE: 1998-09-04
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EARLIER APPLICATION NUMBER: 60/040,33
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PRIOR APPLICATION NUMBER: 60/056,632
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PRIOR APPLICATION NUMBER: 60/056,876
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EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
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PRIOR APPLICATION NUMBER: 60/043,670
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EARLIER APPLICATION NUMBER: 60/043,578 EARLIER TILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,576 EARLIER TILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/047,501 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/043,670 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,632 EARLIER APPLICATION NUMBER: 60/056,632 EARLIER APPLICATION NUMBER: 60/056,664 EARLIER APPLICATION NUMBER: 60/056,664	APPLICATION FILING DATE: APPLICATION APPLICATION	FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047, FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/057, FILING DATE: 05-86P-1997 APPLICATION NUMBER: 60/047, FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/056,894 EARLIER APPLICATION NUMBER: 60/056,911 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,874 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,810 EARLIER APPLICATION NUMBER: 60/056,864 EARLIER APPLICATION NUMBER: 60/056,864 EARLIER APPLICATION NUMBER: 60/056,631 EARLIER APPLICATION NUMBER: 60/056,631 EARLIER APPLICATION NUMBER: 60/056,631 EARLIER APPLICATION NUMBER: 60/056,645	R FILING DATE: 1997-0: R APPLICATION NUMBER:

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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
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EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-26
EARLIER FILING DATE: 1997-08-26
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EARLIER FILING DATE: 1997-08-22
NUMBER: 05 SEQ ID NO 64
LENGTH: 2033
                                                         CURRENT FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 09/148,545
PRIOR APPLICATION NUMBER: 09/040,162
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,161
PRIOR APPLICATION NUMBER: 60/040,161
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,626
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PRIOR APPLICATION NUMBER: 60/040,163
PRIOR APPLICATION NUMBER: 60/047,615
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US-09-981-876-120/c
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TITLE OF INVENTION: 70 Human
FILE REFERENCE: PZ001P1
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Pred. No. 1.3e+02;
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PRIOR FILLING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,592
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PRIOR APPLICATION NUMBER: 60/047,598
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PRIOR PILLING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,598
PRIOR APPLICATION NUMBER: 60/047,612
PRIOR APPLICATION NUMBER: 60/043,514
PRIOR APPLICATION NUMBER: 60/043,514
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PRIOR APPLICATION
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PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,618
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,503
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OR APPLICATION NUMBER: 60/056,910
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,864
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,631
OR FILING DATE: 1997-08-22
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OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/057,761
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OR APPLICATION NUMBER: 60/047,599
OR APPLICATION NUMBER: 60/047,599
OR APPLICATION NUMBER: 1997-05-23
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APPLICATION NUMBER: 60/047,585
PITTING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,588
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FILING DATE: 1997-08-22
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FILING DATE: 1997-04-11
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60/047,503

60/047,618 60/047,617 60/047,583 60/047,633

FILING DATE: 1997-UJ L APPLICATION NUMBER: 60 APPLICATION NUMBER: 605-1

1997-05-23

APPLICATION NUMBER:

60/047,502

APPLICATION NUMBER: 60/ FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ FILING DATE: 1997-05-23

60/047,597

60/047,600 60/047,615 60/040,163

FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/
FILING DATE: 1997-05-23

APPLICATION NUMBER: 60/040,336 FILING DATE: 1997-03-07

APPLICATION NUMBER:

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SOFTWARE: PatentIn Ver.
SEQ ID NO 120
LENGTH: 2136
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PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
114 ATATTAACGTCCATGTTCTC 95
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OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,908
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/048,964
OR FILING DATE: 1997-06-06
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FILING DATE: 1997-08-22
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RESULT 10 US-09-148-545-120/c CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: POT/US
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EARLIER FILING DATE: 1997-03-07
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EARLIER APPLICATION NUMBER: 60/04
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EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07 Sequence 120, Fublication No. CURRENT APPLICATION NUMBER: FILE REFERENCE: PZ001P1 APPLICATION NUMBER: 60/040,161 FILING DATE: 1997-03-07 APPLICATION NUMBER: 60/040,626 Application US/09148545 o. US20030027132A1 o et al. 60/040,333 60/040,162 US/09/148,545 60/038,621 60/040,334 PCT/US98/04482 Secreted Proteins

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US-09-820-893-44/c
               TITLE OF INVENTION: Molecular Toxicology Modeling FILE REFERENCE: 44921-5038 US
CURRENT APPLICATION UNMERR: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION UNMER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
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EARLIER APPLICATION NUMBER: 60/056,884
EARLIER TILING DATE: 1997-08-22
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SEQ ID NO 120
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GENERAL INFORMATION:
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                                                                                                                                                                                                                APPLICANT:
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/531,119
PRIOR FILING DATE: 2000-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/102,895
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: 31 Human Secreted Proteins
FILE REFERENCE: PZ033P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
                                                                                                                                                                                                                                                                     APPLICANT: Mendrick, Donna APPLICANT: Porter, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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Local Similarity 85.0%;
les 17; Conservation
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APPLICATION NUMBER: US 60/290,645
                                                                                                                                                                                             Johnson, Kory
Castle, Arthur
Elashoff, Michael
Gene Logic, Inc.
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Pred. No. 1.
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Pred. No. 1
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PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
                                                                                                                                                                                                                 2000-06-30
2000-09-01
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 40
LENGTH: 6061
TYPE: DNA
                                                                      Query Match
Best Local S
Matches 17
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SEQ ID NO 1469
LENGTH: 2196
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CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
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PRIOR FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OLEK, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1054 ATCTTCACGCCCACGGTCTC 1035
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2190 ATATTAACGTCAACGTTCTC
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                   1 ATATTAACGCCCACGCTCTC 20
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                                                                        l Similarity
17; Conser
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85.0%; Pred. No. 1.
                                                                                        76.0%; Score 15.2;
85.0%; Pred. No. 1
 2171
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3;
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                                                                                                             Length 6061;
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RESULT 14 US-09-738-626-1562

; Sequence 1562, Application US/09738626

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; TYPE: DNA ; ORGANISM: Corynebacterium glutamicum US-09-738-626-1562
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR ELIMG DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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SEQ ID NO 1562
LENGTH: 873
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Best Local :
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APPLICANT:
APPLICANT:
                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1

CURRENT APPLICATION NUMBER: US/09/944,413

CURRENT FILING DATE: 2001-09-26

FRIOR APPLICATION NUMBER: 09/866,028

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: DOCEMBER: 60/067,411

PRIOR PILING DATE: December 3, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR PILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR PILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069335
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APPLICANT: Botstein, David
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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APPLICANT: MIZOGUCHI, HIROS
APPLICANT: ANDO, SEIKO
       PRIOR FILING DATE:
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579 TAATAACGCCCACGCGCT 596
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5. US20020156004A1
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TATEISHI, NAOKO
SENOH, AKIHIRO
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Hillan, Kenneth
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OCHIAI, KEIKO
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     December 11,
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Pred. No. 1.9e+02;
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                            NUMBER OF SEQ ID N
SEQ ID NO 54
LENGTH: 2331
TYPE: DNA
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PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION UMMBER: 09/218,517
PRIOR PRIOR APPLICATION UMMBER: 22, 1998
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PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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PRIOR APPLICATION NUMBER: PCT/USS9/21090
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/USS9/28409
PRIOR FILING DATE: No. US20020156004Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/USS9/28313
PRIOR FILING DATE: No. US20020156004Alember 30, 1999
                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: MAY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: February PRIOR APPLICATION NUMBER: PC PRIOR FILING DATE: March 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
TYPE: DNA ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 60/16,222
OR FILING DATE: July 28, 1999
OR APPLICATION NUMBER: PCT/US98/19330
OR FILING DATE: September 16, 1998
OR APPLICATION NUMBER: PCT/US98/25108
OR FILING DATE: December 1, 1998
OR FILING DATE: December 1, 1998
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OR APPLICATION NUMBER: 60/074,086
OR FILING DATE: FEBRUARY 9, 1998
OR APPLICATION NUMBER: 60/074,092
OR FILING DATE: FEBRUARY 9, 1998
OR APPLICATION NUMBER: 60/075,945
OR FILING DATE: FEBRUARY 25, 1998
OR APPLICATION NUMBER: 60/112,850
OR APPLICATION NUMBER: 60/113,296
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US00/03565
FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
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FILING DATE: December1, 199
APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
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                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PC FILING DATE: March 30,
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ALIGNMENTS

ACCESSION VERSION KEYWORDS REFERENCE AUTHORS SOURCE ORGANISM COMMENT DEFINITION TITLE JOURNAL BH210086.1 GSS. Use of end sequences from Schistosoma mansoni (Puerto Rico strain)
Sml BAC library for gene discovery and map construction
Unpublished (2001)
Other GSSs: Sml-56700.TR
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208 sequence. BH210086 Schistosoma mansoni Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosomatolea; Lacentae; Schistosomatolea; Schistosomatolea; Schistosomatolea; Digenea; Digenea BH210086 687 Sm1-56J20.TF Sm1 Schistosoma Seq primer: M13 For Class: BAC ends. Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed
,N.M. Schistosoma mansoni. Email: nelsayed@tigr.org lo.edu). GI:16389299 bp DN mansoni DNA NA linear GSS 24-OCT-2001 genomic clone Sm1-56J20, DNA

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SOURCE
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                                                                                                                                                                                                                                                                                     Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdelong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 677 row: C column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618 Fax: (206) 616-3887 Enail: jwallace@u.washington.edu
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1 (bases 1 to 570)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a.
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HS_5101_A1_B08_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=677 Col=15 Row-C, DNA sequence.
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/organism="Homo sapiens"
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/clone="plate=677 Col=15 Row=C"
/clone_Lib="RPCI-11 Human Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40410780 319 bp DNA linear GSS 09-JUN-200 Sheared DNA-57G10.TR Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-57G10, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library Unpublished (1999) Contact: Najib M. El-Sayed Department of Eukaryotic Genomics The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma brucei.
Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through Research Genetics, Alabama, USA. Sheared DNA end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13-Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: nelsayed@tigr.org
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204 c 63 g 127 t 9 others
                                                                                                            Approach, eds
Press, 1999).'
a 56 c
                                                                                                                                                            /note="Wector: pUC18; Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for Whole genome shotpun sequencing projects. In Genome Sequencing: A Practical approach, eds. M. Vaudin and B. Barell, Oxford University
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Trypanosoma brucei"
/strain="TREU927/4 GUTAt 10.1"
/db_xref="TREU927/4"
/clone="Sheared DNA-57G10"
/clone_lib="Gheared DNA"
/clone_lib="Gheared DNA"
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1, .319
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94.7%;
84.0%;
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Score 16.8; DB 17; Pred. No. 5.8e+02;
                                                                                                         93 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://image.llnl.gov
Plate: LLCM1368 row: 1 column: 05
High quality sequence stop: 676.
Location/Qualifiers
                                                                         AV755514
AV755514 BM Homo sapiens
AV755514
AV755514.1 GI:10913362
                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: CLONTECH Laboratories, Inc.
CONA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Constium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 706)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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Mammalia; Eutheria;
                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                             174
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                                                                                                                                                                                                                                                                                                                                                                                                              /Organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="Taxon:9606"
/clone="IMAGE:4615444"
/clone=lib="NIH_MGC.75"
/lab_host="DH10B (TI phage-resistant)"
/noce="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgccteggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCCGACATG-GT(30)BN-3' (Where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

CA) 158 c 191 g 182 t 1 others
                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                           84.0%;
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7.2e+02;
hes 2;
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                                                                                                                  nRNA linear EST 19-OCT-
BMFBGD11 5', mRNA sequence.
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Best Local Similarity
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EST.
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Contact: Zeguang Han
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gu, J., Zhao, M., Huang, Q., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H., Gu, Y., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zen, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gao, G., Wang, Z., Zhang, Q., Chen, S., Han, Z. and Chen, Z. Homo sapiens CDNA BM clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA698952 219 bp mRNA linear EST 19-APR-20
HL06045.5prime HL Drosophila melanogaster head BlueScript
Drosophila melanogaster cDNA clone HL06045 5prime, mRNA sequence.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                 Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720,
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, es
Plate: 60 row: D column: 9
                                                                                                                                                                                                                                                                                                                                           BDGP/HHMI Drosophila EST Project Unpublished (2001)
                                                                                                                                                           High quality sequence stop: 157
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                    Harvey, D., Brokstein, P.,
Lewis, S. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                           Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 219)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Bone marrow"
/cell_type="CD34" hematopoietic stem/progenitor cell"
/lab_host="BM25.8" prriplEx2; Site_1: sfiIA; Site_2: sfiIB"
/note="Vector: prriplEx2; Site_1: sfiIA; Site_2: sfiIB"
189 c 221 g 212 t 5 others
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/clone_lib="BM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                 /clone="HL06045"
/clone_lib="HL Drosophila melanogaster head BlueScript"
/sex="male and female"
/dev_stage="adult"
                                                                                                   /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
'lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:2701881
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90.0%;
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Pred. No. 7
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7.5e+02;
nes 2;
                                                                                                                                                                                                                                                                                                                                                                                                              Evans-Holm, M., Su, C., Tsang, G.,
                                                                                                                                                                                                                           est@fruitfly.berkeley.edu
                                                                                                                                                                                                                                                                    USA
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RESULT 8
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                                                            ATATTAACGCCAACGCTC
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SALK_036819 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_036819, DNA sequence.
BH809948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alonso,J.M., Leissé,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn, Zinmerman,J. and Boker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                         l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis Genome Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: TDNA tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: head--brain & sensory organ; Vector: BlueScript SK; Site_1: EcoRI; Site_2: XhoI; Constructed using Stratagene ZAP-cDNA Synthesis kit. Oligo dT-primed and directionally cloned at EcoRI and XhoI in BlueScript SK(+/-)"

8 54 c 58 g 59 t
                                                                                                                                                                                                                                       /clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 69 c 53 g 91 t
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/clone="SALK_036819"
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/strain="Columbia 0"
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Pred. No. 8.3e+02;
0; Mismatches 1;
                                                                                                                                                           Score 16.4; DB 17;
Pred. No. 9e+02;
                                                                                                                                            Mismatches
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Harvey, D., Brokstein, P., Hong, L.,
Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                 Anderson, J.V. and Horvath, D.P.
Identification of mRNAs expressed in underground adventitious buds of Euphorbia esula (leafy spurge)
Unpublished (2000)
Contact: Anderson JV
Plants Science Research
                                                                                                                                                        Euphorbia esula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Malpighiales; Euphorbiaceae; Euphorbia.
                                                                                                                                                                                                                                                                                                                        BI962036 573 bp
01231 leafy spurge Lambda HybriZAP
Library Euphorbia esula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720,
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA698954.1 GI:2701883
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                                                                                                                                                                                                                                                                        EST
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USDA/ARS, Biosciences Research Lab
1605 Albrecht Blvd., PO Box 5674, 1
                                                                                                                                                                                                                                                                                           B1962036.1
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                                                                                                                                                  (bases 1 to 573)
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Location/Qualifiers
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60 row: D column: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: head--brain & sensory organ; Vector: BlueScript SK; Site_1: ECORI; Site_2: XhOI; Constructed using Stratagene 2AP-cDNA Synthesis kit. Oligo dT-primed and directionally cloned at ECORI and XhOI in BlueScript SK(+/-)" 85 g 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="HL Drosophila melanogaster head /sex="male and female" /dev_stage="adult" /lab_host="SOLR"
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/db_xref="taxon:7227"
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94.4%;
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Fargo,
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2 TATTAACGCCCACGCTCTC 20
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17; Conserv
                               l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecular Basis of Wood Formation
Unpublished (2000)
Contact: Johnson, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM133610 679 bp mRNA linear EST 07-JAN-2002 NXLV_009_F09_F NXLV (NSf Xylem Late wood Vertical) Pinus taeda cDNA close NXLV_009_F09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                           Email: ajohnson@unity.ncsu.edu Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Stre
Spermatophyta; Coniferopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pinus taeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM133610.1 GI:17140689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: andersjv@fargo.ars.usda.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oblolly pine.
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919 515 7800
919 515 7801
                               Conservative
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                                                                                                     /note="Vector: pTriplEx; Site_1: EcoRI; The library is from late (summer-August) wood, taken from below the crown of a 20 year old tree. The harvested xylem tissue was on the the cusp between transitional and mature wood. NOTE: The sequences contain a 'CDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCCXTTATGGCC'."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="16AR"
/clone_lib="leafy spurge Lambda HybriZAP 2.1 two-hybrid
vector cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="underground adventitious buds"
/dev_stage="3-day induced (decapitated)"
152 c 129 g 155 t 3 others
                                                                                                                                                                                                                                 /strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXIV_009 r909"
/clone_lib="NXIV (Nsf Xylem Late wood Vertical)"
/tlssue_type="primary xylem"
/dev_stage="late wood"
/lab_host="XLI-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Euphorbia esula"
/db_xref="taxon:3993"
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                                            Score 16.4; DB 13
Pred. No. 1.1e+03;
                               Mismatches
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ida; Coniferales; Pinaceae; Pinus; Pinus.
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                                                           DB 13;
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Query Match
Best Local
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                                                                                            sequence.
AA950399
AA950399.2
                                                                                                                                           AA950399
872 bp mRNA Linear Transcription of the LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD28939 5 similar to C68240; FBan0008240 melanogaster cDNA clone LD28939 5 similar to C68240; FBan0008240 mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
On May 1, 1998 this sequence version replaced Other_ESTs: LD23315.3prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.
BDGF/HHMI Drosophila EST Project
  Drosophila melanogaster
Eukaryota; Metazoa; Art
                                                                        EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: http://www.fruitfly.org/EST, est@fruitfl
hit genomic AE003506: arm:X [1729.1364,17592357]
estimated-cyto:16B4-16D6: 04/10/2001
Plate: LD.233 row: B column: 3
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila.
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                                                 fruit fly.
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One Cyclotron Rd, Berkeley, CA 94720,
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pOT2. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="LD Drosophila melanogaster embryo p0T2"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2
XhoI; Sized fractionated cDNAs were directly ligated into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="XL1 Blue"
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/db_xref="taxon:7227"
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Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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94.4%;
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Pred. No. 1
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ACCESSION
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AQ752099/c
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Best Local Similarity
77 17; Conserve
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HS_5570_B2_G10_T7& RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1146 Col=20 Row=N, DNA sequence.
AQ752099
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1503)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Malar,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798

Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic AE003506: arm:X [17291364,17592357] estimated-cyto:16B4-16D6: 04/10/2001

Plate: LD.889 row: D column: 3
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                                                                                                                   High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
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One Cyclotron Rd, Berkeley, CA 94720, USA
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                                                                                                                                                           Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ752099.1 GI:5539257
ux: (206) 616-387
nail: jwallace@u.washington.edu
noil: jwallace@u.washington.edu
lones are derived from the human BAC library RPCI-11.
library availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 872)
                                                                             Queen Anne Avenue North, Seattle, (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220
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224 c
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Xhol; Sized fractionated cDNAs were directly ligated into
pOT2.
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/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
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/db_xref="taxon:7227"
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Pred. No. 1.2e+03;
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                                                                                                    WA 98109,
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TITLE
      Query Match
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206 ATTAACGCCCACCCTCTC 189
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                                                                                                                                                                                                                                                                                                                 2 (Dases I to 940).

Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J. Direct Submission

Direct Submission

Submitted (16:FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr Roux, Paris 75015, France

This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryo
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSOlMAP 240 bp DNA linear Anopheles gambiae GSS T7 end of clone 21F09 of Not from strain PEST of Anopheles gambiae (African mal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: T7
Class: BAC ends
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Plate: 1146 row: N column: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic survey sequence.
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                                                                                                                                                                                                                                                                                                    Pasteur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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1 (bases 1 to 940)
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a 311 c 520 g 197 t 23 others
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1. .940
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/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                   /clone_lib="NotreDame1"
/note="end : T7"
131 c 276 g 2
                                                                                                                                              /organism="Anopheles gambiae"
/strain="pBST"
/db_xref="taxon:7165"
/clone="21F09"
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80.0%;
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Pred. No. 1.4e+03;
0; Mismatches 1;
Score 16;
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17;
Length 940;
                                                                           27 others
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Search completed: May 12, 2003, 02:35:28
Job time: 249.143 secs
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                  Matches 16; Conservative
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E 1 (bases 1 to 1161)

NIH-MGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact; Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ067992 1161 bp mRNA linear EST 02-APR-2002
AGENCOURT_6792474 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5768997
5', mRNA sequence.
BQ067992
BQ067992.1 GI:19897038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://image.llnl.gov
Plate: LLAM12829 row: 1 column: 22
High quality sequence stop: 440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
//db_xref="taxon:9606"
//clone="IMAGE:5768997"
//clone_lib="NIH_MGC_121"
//lab_host="DH10B"
//lab_host
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2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                       Score 16; DB 14; Length 1161; Pred. No. 2e+03;
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